SCORE Search Results Details for Application 09556178 and Search Result 20101214_103254_us-09-556-178-5.rag.

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This page gives you Search Results detail for the Application 09556178 and Search Result 20101214_103254_us-09-556-178-5.rag.

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                          GenCore version 6.3
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OM protein - protein search, using sw model

Run on:          December 14, 2010, 11:22:17 ; Search time 37 Seconds
                                            (without alignments)
                                            5898.160 Million cell updates/sec

Title:           US-09-556-178-5
Perfect score:   882
Sequence:        1 MEALILEPSLYTVKAILILD.........QTVSQVLQSAKEQIKWSLLR 177

Scoring table:   BLOSUM62
                 Gapop 10.0 , Gapext 0.5

Searched:        6395994 seqs, 1224146475 residues

Total number of hits satisfying chosen parameters:      6395994

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :        A_Geneseq_201023:*
                 1:  geneseqp1:*
                 2:  geneseqp2:*
                 3:  geneseqp3:*
                                    SUMMARIES
                 %
Result           Query
   No.    Score  Match Length DB  ID                          Description
 ------------------------------------------------------------------------
     1      882  100.0    177  1  AAY49960                    Aay49960 Human ves
     2      882  100.0    177  1  AAB03815                    Aab03815 Human ves
     3      882  100.0    177  1  AAB03789                    Aab03789 Human cap
     4      882  100.0    177  1  ADO23737                    Ado23737 COPI coat
     5      882  100.0    177  2  AEJ65021                    Aej65021 Liver can
     6      882  100.0    177  3  AYI11804                    Ayi11804 Human coa
     7      845   95.8    177  1  ADO57263                    Ado57263 Kidney de
     8      673   76.3    210  1  AAY31641                    Aay31641 Human tra
     9      673   76.3    210  1  ADO23725                    Ado23725 COPI coat
    10      673   76.3    210  3  AYI11805                    Ayi11805 Human coa
    11      671   76.1    137  1  AAG01470                    Aag01470 Human sec
    12      580   65.8    185  1  ADO21857                    Ado21857 Human ves
    13    564.5   64.0    160  1  ABB60295                    Abb60295 Drosophil
    14    564.5   64.0    160  2  AFB87634                    Afb87634 Fruit fly
```

15	507.5	57.5	181	2	ARO36046	Aro36046 Soybean c
16	507.5	57.5	181	2	ARO37763	Aro37763 Soybean c
17	507.5	57.5	181	3	AXJ10909	Axj10909 Heteroder
18	507.5	57.5	181	3	AXJ09192	Axj09192 Heteroder
19	493.5	56.0	175	2	ADY65214	Ady65214 S. manson
20	441.5	50.1	154	2	ARO39451	Aro39451 Soybean c
21	441.5	50.1	154	3	AXJ12597	Axj12597 Heteroder
22	440	49.9	99	1	AAB54324	Aab54324 Human pan
23	394	44.7	179	2	AFQ47080	Afq47080 Glycine m
24	386	43.8	177	2	ARM90905	Arm90905 Arabidops
25	386	43.8	177	2	ARM94661	Arm94661 Arabidops
26	379	43.0	177	2	ARB02835	Arb02835 Cotton pr
27	375.5	42.6	180	1	AFP84367	Afp84367 Glycine m
28	373	42.3	182	2	ARL84894	Arl84894 Maize pla
29	371	42.1	182	1	AAG35416	Aag35416 Zea mays
30	371	42.1	182	2	ALJ76006	Alj76006 Plant pro
31	371	42.1	182	2	AFC59274	Afc59274 Maize ami
32	371	42.1	182	2	ARM13352	Arm13352 Zea mays
33	371	42.1	182	3	AYF39857	Ayf39857 Plant pol
34	371	42.1	206	1	ADX78919	Adx78919 Plant ful
35	371	42.1	206	2	ANO11441	Ano11441 Zea mays
36	371	42.1	225	1	ADY23237	Ady23237 Plant ful
37	371	42.1	225	2	ANO34177	Ano34177 Zea mays
38	368	41.7	179	1	AAG38559	Aag38559 Arabidops
39	368	41.7	179	2	ALJ80333	Alj80333 Plant pro
40	368	41.7	179	2	ARN03104	Arn03104 Arabidops
41	368	41.7	225	2	ARN03103	Arn03103 Arabidops
42	364	41.3	182	2	ARM52453	Arm52453 Glycine m
43	359	40.7	177	1	ADT60317	Adt60317 Plant pol
44	359	40.7	177	2	AFC50108	Afc50108 Wheat ami
45	359	40.7	177	2	AJG83201	Ajg83201 Triticum

ALIGNMENTS

```
RESULT 1
AAY49960
ID   AAY49960 standard; protein; 177 AA.
XX
AC   AAY49960;
XX
DT   15-JUN-2007  (revised)
DT   04-FEB-2000  (first entry)
XX
DE   Human vesicle trafficking protein 3.
XX
KW   Human; vesicle trafficking protein; VTP-1; VTP-2; VTP-3; apoptosis;
KW   cancer; inflammation; BOND_PC; coatomer protein complex, subunit zeta 1;
KW   CGI-120 protein; coatomer protein complex, subunit zeta 1 [Homo sapiens];
KW   COPZ1; COPZ; CGI-120; zeta1-COP; subunit zeta;
KW   nonclathrin coat protein zeta1-COP;
KW   coatomer protein complex, subunit zeta 1 [Mus musculus]; D4Ertd360e;
KW   5930435A22Rik; AA407760; MGC118060;
KW   similar to Coatomer zeta-1 subunit (Zeta-1 coat protein) (Zeta-1 COP);
KW   LOC609925; LOC607013;
KW   coatomer protein complex, subunit zeta 1, isoform CRA_a;
KW   coatomer protein complex, subunit zeta 1, isoform CRA_a [Homo sapiens];
KW   unnamed protein product; unnamed protein product [Mus musculus];
KW   hypothetical protein; hypothetical protein [Pongo pygmaeus]; HSPC181;
KW   HSPC181 [Homo sapiens]; z-cop; z-cop [Homo sapiens];
KW   Coatomer protein complex, subunit zeta 1 [Homo sapiens];
KW   CGI-120 protein [Homo sapiens]; zeta1-COP [Homo sapiens];
KW   unnamed protein product [Macaca fascicularis];
KW   Coatomer protein complex, subunit zeta 1 [Mus musculus];
KW   nonclathrin coat protein zeta-COP;
KW   nonclathrin coat protein zeta-COP [Mus musculus]; Copz1 protein;
```

```
KW   Copz1 protein [Mus musculus]; GO5783; GO6886; GO6888; GO6890; GO6891;
KW   GO16020; GO30126; GO30662; GO5198; GO8565.
XX
OS   Homo sapiens.
XX
PN   US5989859-A.
XX
PD   23-NOV-1999.
XX
PF   07-NOV-1997;   97US-00967364.
XX
PR   07-NOV-1997;   97US-00967364.
XX
PA   (INCY-) INCYTE PHARM INC.
XX
PI   Bandman O,  Guegler KJ,  Corley NC,  Lal P,  Shah P;
XX
DR   WPI; 2000-022782/02.
DR   N-PSDB; AAZ35835.
DR   PC:NCBI; gi7706337.
DR   PC:SWISSPROT; P61923, P61924, Q5R5F2.
DR   PC:BIND; 54453.
XX
PT   Novel vesicle trafficking proteins used in the diagnosis, prevention, and
PT   treatment of inflammation or cancer.
XX
PS   Claim 9; Fig 7; 55pp; English.
XX
CC   The present sequence represents the human vesicle trafficking protein
CC   designated VTP-3. VTPs can be used in a method for preventing or treating
CC   disease associated with an increase in apoptosis. The method can treat
CC   diseases such as cancer and inflammation, by administering a VTP
CC   antagonist
CC
CC   Revised record issued on 15-JUN-2007 : Enhanced with precomputed
CC   information from BOND.
XX
SQ   Sequence 177 AA;

  Query Match             100.0%;  Score 882;  DB 1;  Length 177;
  Best Local Similarity   100.0%;
  Matches  177;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MEALILEPSLYTVKAILILDNDGDRLFAKYYDDTYPSVKEQKAFEKNIFNKTHRTDSEIA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MEALILEPSLYTVKAILILDNDGDRLFAKYYDDTYPSVKEQKAFEKNIFNKTHRTDSEIA 60

Qy         61 LLEGLTVVYKSSIDLYFYVIGSSYENELMLMAVLNCLFDSLSQMLRKNVEKRALLENMEG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LLEGLTVVYKSSIDLYFYVIGSSYENELMLMAVLNCLFDSLSQMLRKNVEKRALLENMEG 120

Qy        121 LFLAVDEIVDGGVILESDPQQVVHRVALRGEDVPLTEQTVSQVLQSAKEQIKWSLLR 177
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 LFLAVDEIVDGGVILESDPQQVVHRVALRGEDVPLTEQTVSQVLQSAKEQIKWSLLR 177


RESULT 2
AAB03815
ID   AAB03815 standard; protein; 177 AA.
XX
AC   AAB03815;
XX
DT   15-JUN-2007  (revised)
DT   13-OCT-2000  (first entry)
XX
DE   Human vesicle trafficking protein-3 (VTP-3) amino acid sequence.
XX
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KW   Vesicle trafficking protein; VTP-3; human; cancer; inflammation; asthma;
KW   foetal development; Crohn's disease; diabetes; multiple sclerosis;
KW   rheumatoid arthritis; infection; ulcerative colitis; proliferation;
KW   irritable bowel syndrome; apoptosis; AIDS; Alzheimer's disease;
KW   Parkinson's disease; osteoporosis; wasting disorder; BOND_PC;
KW   coatomer protein complex, subunit zeta 1; CGI-120 protein;
KW   coatomer protein complex, subunit zeta 1 [Homo sapiens]; COPZ1; COPZ;
KW   CGI-120; zeta1-COP; subunit zeta; nonclathrin coat protein zeta1-COP;
KW   coatomer protein complex, subunit zeta 1 [Mus musculus]; D4Ertd360e;
KW   5930435A22Rik; AA407760; MGC118060;
KW   similar to Coatomer zeta-1 subunit (Zeta-1 coat protein) (Zeta-1 COP);
KW   LOC609925; LOC607013;
KW   coatomer protein complex, subunit zeta 1, isoform CRA_a;
KW   coatomer protein complex, subunit zeta 1, isoform CRA_a [Homo sapiens];
KW   unnamed protein product; unnamed protein product [Mus musculus];
KW   hypothetical protein; hypothetical protein [Pongo pygmaeus]; HSPC181;
KW   HSPC181 [Homo sapiens]; z-cop; z-cop [Homo sapiens];
KW   Coatomer protein complex, subunit zeta 1 [Homo sapiens];
KW   CGI-120 protein [Homo sapiens]; zeta1-COP [Homo sapiens];
KW   unnamed protein product [Macaca fascicularis];
KW   Coatomer protein complex, subunit zeta 1 [Mus musculus];
KW   nonclathrin coat protein zeta-COP;
KW   nonclathrin coat protein zeta-COP [Mus musculus]; Copz1 protein;
KW   Copz1 protein [Mus musculus]; GO5783; GO6886; GO6888; GO6890; GO6891;
KW   GO16020; GO30126; GO30662; GO5198; GO8565.
XX
OS   Homo sapiens.
XX
PN   US6071703-A.
XX
PD   06-JUN-2000.
XX
PF   04-AUG-1999;   99US-00368408.
XX
PR   07-NOV-1997;   97US-00967364.
XX
PA   (INCY-) INCYTE PHARM INC.
XX
PI   Guegler KJ,  Shah P,  Corley NC,  Bandman O,  Lal P;
XX
DR   WPI; 2000-422079/36.
DR   N-PSDB; AAA59875.
DR   PC:NCBI; gi7706337.
DR   PC:SWISSPROT; P61923, P61924, Q5R5F2.
DR   PC:BIND; 54453.
XX
PT   Identifying polynucleotides encoding vesicle trafficking proteins (VTP)
PT   for treating and preventing e.g. inflammation, by detecting a
PT   hybridization complex of a nucleic acid from a sample and a
PT   polynucleotide encoding a VTP.
XX
PS   Claim 1; Fig 7; 55pp; English.
XX
CC   This sequence represents a human vesicle trafficking protein (VTP-3)
CC   amino acid sequence. VTP-3 encoding cDNA was isolated from an aortic
CC   tissue cDNA library (HEAONOT03). VTP-3 has structural and chemical
CC   homology with a subunit of cow coatomer protein, zeta COP. The present
CC   invention relates to a method for detecting human VTP encoding
CC   polynucleotide sequences and includes nucleotide and protein sequences
CC   for human VTP-1, VTP-2 and VTP-3. Northern analysis of VTP-1, 2, and 3
CC   shows that their expression is associated with cancer, inflammation and
CC   foetal/infant development. The method of the invention is useful for
CC   screening and identifying a polynucleotide encoding a human VTP, which
CC   may be used for the diagnosis, prevention, or treatment of inflammation
CC   associated disorder, e.g. asthma, Crohn's disease, diabetes, multiple
CC   sclerosis, rheumatoid arthritis, infections, ulcerative colitis and
CC   irritable bowel syndrome. Other diseases and disorders identified,
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CC   prevented or treated with polynucleotide sequences encoding VTP include
CC   those associated with cell proliferation or apoptosis, such as AIDS,
CC   Alzheimer's disease, Parkinson's disease, osteoporosis, wasting diseases
CC   and cancer
CC
CC   Revised record issued on 15-JUN-2007 : Enhanced with precomputed
CC   information from BOND.
XX
SQ   Sequence 177 AA;

  Query Match             100.0%;  Score 882;  DB 1;  Length 177;
  Best Local Similarity   100.0%;
  Matches  177;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MEALILEPSLYTVKAILILDNDGDRLFAKYYDDTYPSVKEQKAFEKNIFNKTHRTDSEIA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MEALILEPSLYTVKAILILDNDGDRLFAKYYDDTYPSVKEQKAFEKNIFNKTHRTDSEIA 60

Qy         61 LLEGLTVVYKSSIDLYFYVIGSSYENELMLMAVLNCLFDSLSQMLRKNVEKRALLENMEG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LLEGLTVVYKSSIDLYFYVIGSSYENELMLMAVLNCLFDSLSQMLRKNVEKRALLENMEG 120

Qy        121 LFLAVDEIVDGGVILESDPQQVVHRVALRGEDVPLTEQTVSQVLQSAKEQIKWSLLR 177
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 LFLAVDEIVDGGVILESDPQQVVHRVALRGEDVPLTEQTVSQVLQSAKEQIKWSLLR 177


RESULT 3
AAB03789
ID   AAB03789 standard; protein; 177 AA.
XX
AC   AAB03789;
XX
DT   15-JUN-2007  (revised)
DT   26-OCT-2000  (first entry)
XX
DE   Human capsid protein zeta-COP amino acid sequence.
XX
KW   Human; capsid-protein; zeta-COP; BOND_PC;
KW   coatomer protein complex, subunit zeta 1; CGI-120 protein;
KW   coatomer protein complex, subunit zeta 1 [Homo sapiens]; COPZ1; COPZ;
KW   CGI-120; zeta1-COP; subunit zeta; nonclathrin coat protein zeta1-COP;
KW   coatomer protein complex, subunit zeta 1 [Mus musculus]; D4Ertd360e;
KW   5930435A22Rik; AA407760; MGC118060;
KW   similar to Coatomer zeta-1 subunit (Zeta-1 coat protein) (Zeta-1 COP);
KW   LOC609925; LOC607013;
KW   coatomer protein complex, subunit zeta 1, isoform CRA_a;
KW   coatomer protein complex, subunit zeta 1, isoform CRA_a [Homo sapiens];
KW   unnamed protein product; unnamed protein product [Mus musculus];
KW   hypothetical protein; hypothetical protein [Pongo pygmaeus]; HSPC181;
KW   HSPC181 [Homo sapiens]; z-cop; z-cop [Homo sapiens];
KW   Coatomer protein complex, subunit zeta 1 [Homo sapiens];
KW   CGI-120 protein [Homo sapiens]; zeta1-COP [Homo sapiens];
KW   unnamed protein product [Macaca fascicularis];
KW   Coatomer protein complex, subunit zeta 1 [Mus musculus];
KW   nonclathrin coat protein zeta-COP;
KW   nonclathrin coat protein zeta-COP [Mus musculus]; Copz1 protein;
KW   Copz1 protein [Mus musculus]; GO5783; GO6886; GO6888; GO6890; GO6891;
KW   GO16020; GO30126; GO30662; GO5198; GO8565.
XX
OS   Homo sapiens.
XX
PN   CN1248624-A.
XX
PD   29-MAR-2000.
XX
PF   22-SEP-1998;   98CN-00119744.
```

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XX
PR   22-SEP-1998;   98CN-00119744.
XX
PA   (XINH-) XINHUANGPU FUDAN GENE ENG CO LTD SHANGHA.
XX
PI   Yu L,  Tu Q,  Fu Q;
XX
DR   WPI; 2000-431993/38.
DR   N-PSDB; AAA59847.
DR   PC:NCBI; gi7706337.
DR   PC:SWISSPROT; P61923, P61924, Q5R5F2.
DR   PC:BIND; 54453.
XX
PT   Novel human capsid protein subunit coding sequence.
XX
PS   Claim 2; Fig 2; 21pp; Chinese.
XX
CC   This invention relates to a human gene encoding a capsid protein zeta
CC   subunit (zeta-COP). The invention also relates to a zeta-COP protein
CC   sequence. The present sequence represents the human zeta-COP protein
CC   sequence
CC
CC   Revised record issued on 15-JUN-2007 : Enhanced with precomputed
CC   information from BOND.
XX
SQ   Sequence 177 AA;

  Query Match             100.0%;  Score 882;  DB 1;  Length 177;
  Best Local Similarity   100.0%;
  Matches  177;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MEALILEPSLYTVKAILILDNDGDRLFAKYYDDTYPSVKEQKAFEKNIFNKTHRTDSEIA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MEALILEPSLYTVKAILILDNDGDRLFAKYYDDTYPSVKEQKAFEKNIFNKTHRTDSEIA 60

Qy         61 LLEGLTVVYKSSIDLYFYVIGSSYENELMLMAVLNCLFDSLSQMLRKNVEKRALLENMEG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LLEGLTVVYKSSIDLYFYVIGSSYENELMLMAVLNCLFDSLSQMLRKNVEKRALLENMEG 120

Qy        121 LFLAVDEIVDGGVILESDPQQVVHRVALRGEDVPLTEQTVSQVLQSAKEQIKWSLLR 177
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 LFLAVDEIVDGGVILESDPQQVVHRVALRGEDVPLTEQTVSQVLQSAKEQIKWSLLR 177


RESULT 4
ADO23737
ID   ADO23737 standard; protein; 177 AA.
XX
AC   ADO23737;
XX
DT   15-JUN-2007  (revised)
DT   01-JUL-2004  (first entry)
XX
DE   COPI coatomer protein, SEQ ID 26.
XX
KW   Cytostatic; nuclear envelope breakdown; nuclear pore protein; Nupl53;
KW   COPI coatomer complex; cancer; BOND_PC;
KW   coatomer protein complex, subunit zeta 1; CGI-120 protein;
KW   coatomer protein complex, subunit zeta 1 [Homo sapiens]; COPZ1; COPZ;
KW   CGI-120; zeta1-COP; subunit zeta; nonclathrin coat protein zeta1-COP;
KW   coatomer protein complex, subunit zeta 1 [Mus musculus]; D4Ertd360e;
KW   5930435A22Rik; AA407760; MGC118060;
KW   similar to Coatomer zeta-1 subunit (Zeta-1 coat protein) (Zeta-1 COP);
KW   LOC609925; LOC607013;
KW   coatomer protein complex, subunit zeta 1, isoform CRA_a;
KW   coatomer protein complex, subunit zeta 1, isoform CRA_a [Homo sapiens];
KW   unnamed protein product; unnamed protein product [Mus musculus];
```

```
KW   hypothetical protein; hypothetical protein [Pongo pygmaeus]; HSPC181;
KW   HSPC181 [Homo sapiens]; z-cop; z-cop [Homo sapiens];
KW   Coatomer protein complex, subunit zeta 1 [Homo sapiens];
KW   CGI-120 protein [Homo sapiens]; zeta1-COP [Homo sapiens];
KW   unnamed protein product [Macaca fascicularis];
KW   Coatomer protein complex, subunit zeta 1 [Mus musculus];
KW   nonclathrin coat protein zeta-COP;
KW   nonclathrin coat protein zeta-COP [Mus musculus]; Copz1 protein;
KW   Copz1 protein [Mus musculus].
XX
OS   Unidentified.
XX
PN   WO2004027381-A2.
XX
PD   01-APR-2004.
XX
PF   17-SEP-2003; 2003WO-US029267.
XX
PR   17-SEP-2002; 2002US-0411248P.
XX
PA   (UTAH ) UNIV UTAH RES FOUND.
XX
PI   Ulmann KS,  Liu J,  Prunuske A,  Dimaano C;
XX
DR   WPI; 2004-340314/31.
DR   N-PSDB; ADO23736.
DR   PC:NCBI; gi4929709.
DR   PC:SWISSPROT; P61923, P61924, Q5R5F2.
DR   PC:BIND; 54453.
XX
PT   New composition comprising a molecule that inhibits nuclear envelope
PT   breakdown, useful in treating cancer, e.g. lymphoma, sarcoma or glioma.
XX
PS   Claim 22; SEQ ID NO 26; 180pp; English.
XX
CC   The present invention relates to a composition comprising a molecule that
CC   inhibits nuclear envelope breakdown by interfering with the interaction
CC   between nuclear pore protein Nupl53 and COPI coatomer complex. The
CC   composition is useful in treating, inhibiting or preventing cancer, e.g.
CC   lymphoma, leukaemia, mycosis fungoide, carcinoma, adenocarcinoma,
CC   sarcoma, glioma, blastoma, neuroblastoma, plasmacytoma, histiocytoma,
CC   melanoma, adenoma, hypoxic tumour, myeloma, AIDS-related lymphoma or AIDS
CC   -related sarcoma or metastatic, bladder, brain or nervous system cancer,
CC   glioblastoma or ovarian, skin or liver cancer, squamous cell carcinomas
CC   of the mouth, throat, larynx, and lung or colon, cervical, breast,
CC   epithelial, renal, genitourinary or pulmonary cancer, oesophageal
CC   carcinoma, head and neck carcinoma or haematopoietic, testicular,
CC   colorectal, prostatic or pancreatic cancer. The present sequence was used
CC   to illustrate the invention.
CC
CC   Revised record issued on 15-JUN-2007 : Enhanced with precomputed
CC   information from BOND.
XX
SQ   Sequence 177 AA;

  Query Match             100.0%;  Score 882;  DB 1;  Length 177;
  Best Local Similarity   100.0%;
  Matches  177;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MEALILEPSLYTVKAILILDNDGDRLFAKYYDDTYPSVKEQKAFEKNIFNKTHRTDSEIA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MEALILEPSLYTVKAILILDNDGDRLFAKYYDDTYPSVKEQKAFEKNIFNKTHRTDSEIA 60

Qy         61 LLEGLTVVYKSSIDLYFYVIGSSYENELMLMAVLNCLFDSLSQMLRKNVEKRALLENMEG 120
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Qy        121 LFLAVDEIVDGGVILESDPQQVVHRVALRGEDVPLTEQTVSQVLQSAKEQIKWSLLR 177
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 LFLAVDEIVDGGVILESDPQQVVHRVALRGEDVPLTEQTVSQVLQSAKEQIKWSLLR 177


RESULT 5
AEJ65021
ID   AEJ65021 standard; protein; 177 AA.
XX
AC   AEJ65021;
XX
DT   15-JUN-2007  (revised)
DT   05-OCT-2006  (first entry)
XX
DE   Liver cancer associated protein SEQ ID NO 63.
XX
KW   protein production; recombinant DNA; liver tumor; cytostatic; neoplasm;
KW   gastrointestinal disease; BOND_PC;
KW   coatomer protein complex, subunit zeta 1; CGI-120 protein;
KW   coatomer protein complex, subunit zeta 1 [Homo sapiens]; COPZ1; COPZ;
KW   CGI-120; zeta1-COP; subunit zeta; nonclathrin coat protein zeta1-COP;
KW   coatomer protein complex, subunit zeta 1 [Mus musculus]; D4Ertd360e;
KW   5930435A22Rik; AA407760; MGC118060;
KW   similar to Coatomer zeta-1 subunit (Zeta-1 coat protein) (Zeta-1 COP);
KW   LOC609925; LOC607013;
KW   coatomer protein complex, subunit zeta 1, isoform CRA_a;
KW   coatomer protein complex, subunit zeta 1, isoform CRA_a [Homo sapiens];
KW   unnamed protein product; unnamed protein product [Mus musculus];
KW   hypothetical protein; hypothetical protein [Pongo pygmaeus]; HSPC181;
KW   HSPC181 [Homo sapiens]; z-cop; z-cop [Homo sapiens];
KW   Coatomer protein complex, subunit zeta 1 [Homo sapiens];
KW   CGI-120 protein [Homo sapiens]; zeta1-COP [Homo sapiens];
KW   unnamed protein product [Macaca fascicularis];
KW   Coatomer protein complex, subunit zeta 1 [Mus musculus];
KW   nonclathrin coat protein zeta-COP;
KW   nonclathrin coat protein zeta-COP [Mus musculus]; Copz1 protein;
KW   Copz1 protein [Mus musculus]; GO5783; GO6886; GO6888; GO6890; GO6891;
KW   GO16020; GO30126; GO30662; GO5198; GO8565.
XX
OS   Homo sapiens.
XX
PN   CN1618808-A.
XX
PD   25-MAY-2005.
XX
PF   21-NOV-2003; 2003CN-10108764.
XX
PR   21-NOV-2003; 2003CN-10108764.
XX
PA   (SHAN-) SHANGHAI HUMAN GENOME RES CENT.
XX
PI   Zhu Z,  Han Z;
XX
DR   WPI; 2005-640540/66.
DR   SWISSPROT; Q9Y3C3.
DR   PC:NCBI; gi7706337.
DR   PC:SWISSPROT; P61923, P61924, Q5R5F2.
DR   PC:BIND; 54453.
XX
PT   Liver cancer related protein and its coding sequence and use.
XX
PS   Claim 1; SEQ ID NO 63; 26pp; Chinese.
XX
CC   The invention describes a novel liver cancer associated protein, the
CC   polynucleotide for coding it, the process for preparing said protein by
CC   recombination, and the application of said polynucleotide. This is the
CC   amino acid sequence of a liver cancer associated protein.
```

```
CC
CC   Revised record issued on 15-JUN-2007 : Enhanced with precomputed
CC   information from BOND.
XX
SQ   Sequence 177 AA;

  Query Match             100.0%;  Score 882;  DB 2;  Length 177;
  Best Local Similarity   100.0%;
  Matches  177;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MEALILEPSLYTVKAILILDNDGDRLFAKYYDDTYPSVKEQKAFEKNIFNKTHRTDSEIA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MEALILEPSLYTVKAILILDNDGDRLFAKYYDDTYPSVKEQKAFEKNIFNKTHRTDSEIA 60

Qy         61 LLEGLTVVYKSSIDLYFYVIGSSYENELMLMAVLNCLFDSLSQMLRKNVEKRALLENMEG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LLEGLTVVYKSSIDLYFYVIGSSYENELMLMAVLNCLFDSLSQMLRKNVEKRALLENMEG 120

Qy        121 LFLAVDEIVDGGVILESDPQQVVHRVALRGEDVPLTEQTVSQVLQSAKEQIKWSLLR 177
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 LFLAVDEIVDGGVILESDPQQVVHRVALRGEDVPLTEQTVSQVLQSAKEQIKWSLLR 177


RESULT 6
AYI11804
ID   AYI11804 standard; protein; 177 AA.
XX
AC   AYI11804;
XX
DT   28-OCT-2010  (first entry)
XX
DE   Human coatomer subunit zeta-1 protein, SEQ ID 29.
XX
KW   Bio-nanoparticle element; Coatomer subunit zeta-1; nanotechnology;
KW   BOND_PC; coatomer protein complex, subunit zeta 1; CGI-120 protein;
KW   COPZ1; COPZ; CGI-120; zeta1-COP; subunit zeta;
KW   nonclathrin coat protein zeta1-COP; D4Ertd360e; 5930435A22Rik; AA407760;
KW   MGC118060;
KW   similar to Coatomer zeta-1 subunit (Zeta-1 coat protein) (Zeta-1 COP);
KW   LOC609925; LOC607013; similar to CGI-120 protein;
KW   PREDICTED: similar to CGI-120 protein [Equus caballus]; LOC100064590;
KW   Copz1_predicted;
KW   similar to Coatomer subunit zeta-1 (Zeta-1-coat protein) (Zeta-1 COP);
KW   LOC100156765; Coatomer subunit zeta-1; DKFZp469A0331;
KW   coatomer protein complex, subunit zeta 1, isoform CRA_a;
KW   unnamed protein product; hypothetical protein; HSPC181; z-cop;
KW   nonclathrin coat protein zeta-COP; Copz1 protein; GO5783; GO6886; GO6888;
KW   GO6890; GO6891; GO16020; GO30126; GO30662; GO5198; GO8565.
XX
OS   Homo sapiens.
XX
PN   US2010226856-A1.
XX
PD   09-SEP-2010.
XX
PF   06-MAR-2009; 2009US-00399906.
XX
PR   06-MAR-2009; 2009US-00399906.
XX
PA   (VITA/) VITALIANO F.
PA   (VITA/) VITALIANO G.
XX
PI   Vitaliano F,  Vitaliano G;
XX
DR   WPI; 2010-L54477/62.
DR   SWISSPROT; P61923.
DR   PC:NCBI; gi7706337.
```

```
DR   PC:SWISSPROT; P61923, P61924, Q5R5F2.
DR   PC:BIND; 54453.
XX
PT   New dynamic bio-nanoparticle element, useful in a multifunction nanoscale
PT   bio-nanoparticle platform, such as a biomedical platform, bio-molecular
PT   platform, electronics platform, and information processing platform.
XX
PS   Claim 1; SEQ ID NO 29; 121pp; English.
XX
CC   The present invention relates to a dynamic bio-nanoparticle element
CC   useful in a multifunction nanoscale bio-nanoparticle platform. The bio-
CC   nanoparticle element comprises a clathrin or coatomer cage subset
CC   element, forming in vitro less than a fully assembled clathrin or
CC   coatomer cage element, having attributes, properties, characteristics,
CC   compositions, behaviors and capabilities, that differ in respect from a
CC   fully assembled clathrin or coatomer cage element and nanoscale elements
CC   of types formed in whole or in part from purified, synthetic or
CC   recombinant amino acid molecule elements and their residue elements. The
CC   invention also provides a method for forming a dynamic bio-nanoparticle
CC   element. The dynamic bio-nanoparticle element is useful in a
CC   multifunction nanoscale bio-nanoparticle platform such as a biomedical
CC   platform, bio-molecular platform, electronics platform and information
CC   processing platform. The dynamic bio-nanoparticle element provides self-
CC   directing, self-replicating, self-adapting, self-repairing, self-
CC   regulating and self-regenerating methods for one or more minimalist, non-
CC   cage elements, which can also perform on-the-fly target prioritization.
CC   The present sequence is a human coatomer subunit zeta-1 protein used in
CC   the method for forming a dynamic bio-nanoparticle element of the
CC   invention.
CC
CC   Revised record issued on 13-OCT-2010 : Enhanced with precomputed
CC   information from BOND.
XX
SQ   Sequence 177 AA;

  Query Match             100.0%;  Score 882;  DB 3;  Length 177;
  Best Local Similarity   100.0%;
  Matches  177;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MEALILEPSLYTVKAILILDNDGDRLFAKYYDDTYPSVKEQKAFEKNIFNKTHRTDSEIA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MEALILEPSLYTVKAILILDNDGDRLFAKYYDDTYPSVKEQKAFEKNIFNKTHRTDSEIA 60

Qy         61 LLEGLTVVYKSSIDLYFYVIGSSYENELMLMAVLNCLFDSLSQMLRKNVEKRALLENMEG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LLEGLTVVYKSSIDLYFYVIGSSYENELMLMAVLNCLFDSLSQMLRKNVEKRALLENMEG 120

Qy        121 LFLAVDEIVDGGVILESDPQQVVHRVALRGEDVPLTEQTVSQVLQSAKEQIKWSLLR 177
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 LFLAVDEIVDGGVILESDPQQVVHRVALRGEDVPLTEQTVSQVLQSAKEQIKWSLLR 177


RESULT 7
ADO57263
ID   ADO57263 standard; protein; 177 AA.
XX
AC   ADO57263;
XX
DT   15-JUN-2007  (revised)
DT   15-JUL-2004  (first entry)
XX
DE   Kidney development associated protein seqid 30.
XX
KW   nephrotropic; cardiant; antiinfertility; cerebroprotective;
KW   neuroprotective; muscular; cytostatic; osteopathic; gene therapy;
KW   kidney development; kidney disorder; developmental disorder;
KW   circulatory disorder; hearing disorder; heart defect; infertility;
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```
KW   stroke; mental retardation; muscle defect; proliferative disorder;
KW   bone defect; bone disorder; zebrafish; BOND_PC; zeta1-cop;
KW   zeta1-cop [Danio rerio]; copz1; CHUNP6876;
KW   nonclathrin coat protein zeta1-COP;
KW   nonclathrin coat protein zeta1-COP [Danio rerio]; GO6810; GO6886;
KW   GO30662; GO8565; GO19012.
XX
OS   Danio rerio.
XX
PN   US2004068763-A1.
XX
PD   08-APR-2004.
XX
PF   28-MAR-2003; 2003US-00403571.
XX
PR   29-MAR-2002; 2002US-0368760P.
XX
PA   (HOPK/) HOPKINS N.
PA   (GOLL/) GOLLING G.
PA   (AMST/) AMSTERDAM A.
PA   (SUNZ/) SUN Z.
XX
PI   Hopkins N,  Golling G,  Amsterdam A,  Sun Z;
XX
DR   WPI; 2004-304692/28.
DR   N-PSDB; ADO57262.
DR   PC:NCBI; gi18858455.
XX
PT   New 459 nucleic acids and encoded polypeptides, useful for diagnosing,
PT   treating or preventing a kidney disorder in an organism, or in screening
PT   for compounds that modulate the development of an organism.
XX
PS   Disclosure; SEQ ID NO 30; 347pp; English.
XX
CC   The invention describes an isolated nucleic acid molecule (I) comprising
CC   a sequence having at least 75% sequence identity to the 459 nucleic acid
CC   sequence of 2808 base pairs (SEQ ID NO: 59) given in the specification,
CC   over at least 600 contiguous base pairs, where the nucleic acid functions
CC   in kidney development. (I) is useful for treating or preventing a kidney
CC   disorder in an organism, where the nucleic acid elicits an alteration in
CC   expression of a 459 nucleic acid sequence in the organism and
CC   subsequently treats or prevents a kidney disorder. The nucleic acid may
CC   also be used in diagnosing, preventing and treating a variety of
CC   mammalian diseases and developmental disorders (e.g. circulatory
CC   disorders, hearing disorders, heart defect, infertility, stroke, mental
CC   retardation, muscle defects, proliferative disorders, or bone defects or
CC   disorders) as well as in screening for compounds that modulate the
CC   development of an organism as a whole or of specific tissues or organs
CC   within that organism. This is the amino acid sequence of a kidney
CC   development associated protein.
CC
CC   Revised record issued on 15-JUN-2007 : Enhanced with precomputed
CC   information from BOND.
XX
SQ   Sequence 177 AA;

  Query Match             95.8%;  Score 845;  DB 1;  Length 177;
  Best Local Similarity   93.2%;
  Matches  165;  Conservative   11;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 MEALILEPSLYTVKAILILDNDGDRLFAKYYDDTYPSVKEQKAFEKNIFNKTHRTDSEIA 60
              |: |||||||||||:||:||||:||:|||||||||:|||||||||||||||||||||||
Db          1 MDTLILEPSLYTVKAVLIMDNDGERLYAKYYDDTYPTVKEQKAFEKNIFNKTHRTDSEIA 60

Qy         61 LLEGLTVVYKSSIDLYFYVIGSSYENELMLMAVLNCLFDSLSQMLRKNVEKRALLENMEG 120
              ||||||||||:||||||||||:|||||||:|||||||||||||||||||||||||||||
Db         61 LLEGLTVVYKSNIDLYFYVIGSSHENELMLMSVLNCLFDSLSQMLRKNVEKRALLENMEG 120
```

```
Qy        121 LFLAVDEIVDGGVILESDPQQVVHRVALRGEDVPLTEQTVSQVLQSAKEQIKWSLLR 177
              ||||||||||||||||||||||||||||:|||||||||:||||||||||||||||
Db        121 LFLAVDEIVDGGVILESDPQQVVHRVALRGDDVPLTEQTVTQVLQSAKEQIKWSLLR 177


RESULT 8
AAY31641
ID   AAY31641 standard; protein; 210 AA.
XX
AC   AAY31641;
XX
DT   02-NOV-1999  (first entry)
XX
DE   Human transport-associated protein-3 (TRANP-3).
XX
KW   Transport-associated protein; TRANP; nuclear pore; nuclear transport;
KW   vesicle trafficking; cancer; cystic fibrosis; multidrug resistance;
KW   hypercholesterolaemia; diagnosis; treatment.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Modified-site   44
FT                   /note= "O-phosphorylated by tyrosine kinase"
FT   Modified-site   45
FT                   /note= "O-phosphorylated by protein kinase C"
FT   Modified-site   55
FT                   /note= "Amidation site"
FT   Modified-site   70
FT                   /note= "O-phosphorylated by casein kinase II or protein
FT                   kinase C"
FT   Modified-site   83
FT                   /note= "N-glycosylated"
FT   Modified-site   85
FT                   /note= "O-phosphorylated by protein kinase C"
FT   Modified-site   86
FT                   /note= "O-phosphorylated by casein kinase II"
FT   Modified-site   88
FT                   /note= "O-phosphorylated by casein kinase II"
FT   Modified-site   111
FT                   /note= "O-phosphorylated by tyrosine kinase"
FT   Modified-site   115
FT                   /note= "O-phosphorylated by casein kinase II"
FT   Modified-site   199
FT                   /note= "O-phosphorylated by casein kinase II or protein
FT                   kinase C"
XX
PN   WO9941373-A2.
XX
PD   19-AUG-1999.
XX
PF   05-FEB-1999;   99WO-US002527.
XX
PR   11-FEB-1998;   98US-00021764.
XX
PA   (INCY-) INCYTE PHARM INC.
XX
PI   Au-Young J,  Hillman JL,  Lal P,  Guegler KJ,  Corley NC,  Yue H;
PI   Bandman O,  Baughn MR;
XX
DR   WPI; 1999-508646/42.
DR   N-PSDB; AAZ11733.
XX
PT   Human TRANP coding sequences, used to treat transport disorders and
PT   cancer.
XX
```

This page gives you Search Results detail for the Application 09556178 and Search Result 20101214_103255_us-09-556-178-5.rpr.

OM protein - protein search, using sw model

Run on: December 14, 2010, 11:24:11 ; Search time 2 Seconds
(without alignments)
7139.284 Million cell updates/sec

Title: US-09-556-178-5
Perfect score: 882
Sequence: 1 MEALILEPSLYTVKAILILD.....QTVSQVLQSAKEQIKWSLLR 177

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	875	99.2	177	2	A49465	coatomer zeta chai
2	499	56.6	184	2	T23002	hypothetical prote
3	344	39.0	162	2	C96635	probable coatomer
4	308	34.9	189	2	S52521	coatomer protein z
5	299.5	34.0	190	2	T41417	coatomer zeta subu
6	267	30.3	153	2	T01831	hypothetical prote
7	141.5	16.0	145	2	T08407	clathrin coat asse
8	118	13.4	143	2	B84581	probable clathrin
9	117	13.3	446	2	S59646	clathrin coat asse
10	116	13.2	194	2	S56796	YAP19 protein homo
11	112.5	12.8	141	2	C71605	clathrin coat asse
12	108	12.2	157	2	T31801	hypothetical prote
13	106.5	12.1	143	2	T40635	clathrin coat asse
14	99	11.2	165	2	S62563	adaptin complex sm
15	98	11.1	1472	2	S67195	probable membrane
16	97.5	11.1	441	2	B49837	clathrin-associate
17	90.5	10.3	214	2	S51405	synaptobrevin SEC2
18	90	10.2	1271	2	T08607	hypothetical prote
19	88.5	10.0	290	2	C96911	transcription regu
20	87.5	9.9	475	2	S65290	clathrin-associate
21	86	9.8	158	2	A40535	clathrin-associate
22	86	9.8	161	2	E84551	clathrin assembly
23	86	9.8	162	2	T06116	probable clathrin-
24	85.5	9.7	663	2	B70460	excinuclease ABC c
25	85.5	9.7	699	2	T18984	hypothetical prote
26	85	9.6	380	2	D64129	probable 8-amino-7
27	84.5	9.6	439	2	S78378	maturase-like prot
28	84.5	9.6	863	2	B72344	tRNA nucleotidyl t
29	84	9.5	132	2	T02991	clathrin coat asse
30	84	9.5	142	2	T15957	hypothetical prote
31	83.5	9.5	412	2	E97736	mitochondrial prot
32	83	9.4	142	2	B40535	clathrin-associate
33	83	9.4	156	2	S37757	clathrin-associate
34	83	9.4	410	2	S64451	hypothetical prote
35	83	9.4	896	2	T47645	centromere protein
36	82.5	9.4	324	2	C90492	hypothetical prote
37	82.5	9.4	569	1	D64215	conserved hypothet
38	82.5	9.4	909	2	AG3314	excinuclease ABC c
39	82.5	9.4	1104	2	S36773	GTPase-activating
40	82	9.3	416	2	D70347	cell division prot
41	82	9.3	659	2	G81334	probable N-acetylm
42	82	9.3	686	2	T23721	hypothetical prote
43	82	9.3	725	2	G90555	vacb-like (shigell
44	82	9.3	803	1	E70041	probable copper-tr
45	82	9.3	1130	2	T21134	hypothetical prote

ALIGNMENTS

RESULT 1
A49465
coatomer zeta chain - bovine
C;Species: Bos primigenius taurus (cattle)
C;Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 09-Jul-2004
C;Accession: A49465
R;Kuge, O.; Hara-Kuge, S.; Orci, L.; Ravazzola, M.; Amherdt, M.; Tanigawa, G.; Wieland, F.T.; Rothman, J.E.
J. Cell Biol. 123, 1727-1734, 1993
A;Title: zeta-COP, a subunit of coatomer, is required for COP-coated vesicle assembly.
A;Reference number: A49465; MUID:94103328; PMID:8276893
A;Accession: A49465
A;Status: preliminary
A;Molecule type: mRNA

```
A;Residues: 1-177 <KUG>
A;Cross-references: UNIPROT:P35604; UNIPARC:UPI0000127EF0; GB:X75935; NID:g441485; PIDN:CAA53539.1; PID:g441486
C;Superfamily: Vesicle coat complex COPI, zeta subunit

  Query Match             99.2%;  Score 875;  DB 2;  Length 177;
  Best Local Similarity   98.9%;
  Matches  175;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 MEALILEPSLYTVKAILILDNDGDRLFAKYYDDTYPSVKEQKAFEKNIFNKTHRTDSEIA 60
              ||||||:|||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MEALILQPSLYTVKAILILDNDGDRLFAKYYDDTYPSVKEQKAFEKNIFNKTHRTDSEIA 60

Qy         61 LLEGLTVVYKSSIDLYFYVIGSSYENELMLMAVLNCLFDSLSQMLRKNVEKRALLENMEG 120
              |||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db         61 LLEGLTVVYKSSIDLYFYVIGSSYENELMLMTVLNCLFDSLSQMLRKNVEKRALLENMEG 120

Qy        121 LFLAVDEIVDGGVILESDPQQVVHRVALRGEDVPLTEQTVSQVLQSAKEQIKWSLLR 177
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 LFLAVDEIVDGGVILESDPQQVVHRVALRGEDVPLTEQTVSQVLQSAKEQIKWSLLR 177


RESULT 2
T23002
hypothetical protein F59E10.3 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T23002
R;Swinburne, J.
submitted to the EMBL Data Library, September 1994
A;Reference number: Z19650
A;Accession: T23002
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-184 <WIL>
A;Cross-references: UNIPROT:O17901; UNIPARC:UPI0000127EF1; EMBL:Z36949; PIDN:CAA85416.1; GSPDB:GN00020; CESP:F59E10.3
A;Experimental source: clone F59E10
C;Genetics:
A;Gene: CESP:F59E10.3
A;Map position: 2
A;Introns: 6/3; 30/3; 60/1; 135/2
C;Superfamily: Vesicle coat complex COPI, zeta subunit

  Query Match             56.6%;  Score 499;  DB 2;  Length 184;
  Best Local Similarity   54.9%;
  Matches   96;  Conservative   44;  Mismatches   29;  Indels    6;  Gaps    3;

Qy          9 SLYTVKAILILDNDGDRLFAKYYD-DTYPSVKEQKAFEKNIFNKTHR-TDSEIALLEGLT 66
              |||::| |:||| ||:|: ||||| |: :|||||||||::|:|| | | ::| ||:|:|
Db         10 SLYSIKGIVILDQDGNRVLAKYYDRTTFGTVKEQKAFEKSLFSKTSRNTSADILLLDGVT 69

Qy         67 VVYKSSIDLYFYVIGSSYENELMLMAVLNCLFDSLSQMLRKNVEKRALLENMEGLFLAVD 126
                 :|:|::|||||:||: |||| | | | ||:|::|| :|||||||:||:::|: : | :|
Db         70 CLYRSNVDLYFYVLGSTRENELFLDATLTCLYDAVSVVLRKNVEKKALIDSMDTIMLIID 129

Qy        127 EIVDGGVILESDPQQVVHRVALRGEDVPLTEQTVSQV----LQSAKEQIKWSLLR 177
              || | |:|:|:| | || | ||: ::|  ::|:|||:    ::|| || |||||:
Db        130 EICDEGIIMETDAQAVVQRTALKSDEVSFSDQSVSQIGFSFMKSANEQFKWSLLK 184


RESULT 3
C96635
probable coatomer zeta subunit T7P1.11 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C;Accession: C96635
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, J.; Altaf, H.; Araujo, R.; Bowman, C.L.; Brooks, S.Y.; Buehler, E.; Chan, A
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.J.; Koo, H.L.; Kremenetskaia, I.; Kurtz, D.B.; Kwan, A.; Lam, B.; Langin-Ho
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, L.J.; Tambunga, G.; Toriumi, M.J.; Town, C.D.; Utterback, T.; van Aken, S.;
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719; PMID:11130712
A;Accession: C96635
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-162 <STO>
A;Cross-references: UNIPROT:Q9C956; UNIPARC:UPI000009CDAC; GB:AE005173; NID:g6751687; PIDN:AAF27670.1; GSPDB:GN00141
C;Genetics:
A;Gene: T7P1.11
A;Map position: 1
C;Superfamily: Vesicle coat complex COPI, zeta subunit

  Query Match             39.0%;  Score 344;  DB 2;  Length 162;
  Best Local Similarity   45.4%;
  Matches   69;  Conservative   33;  Mismatches   44;  Indels    6;  Gaps    2;

Qy         13 VKAILILDNDGDRLFAKYYDDTYPSVKEQKAFEKNIFNKTH----RTDSEIALLEGLTVV 68
              || ||:||::| |:  ||| | :|:   |:||||::| ||     ||: |:  ||   ||
Db          7 VKNILLLDSEGKRVAVKYYSDDWPTNSAQEAFEKSVFTKTQKTNARTEVEVTALENNIVV 66

Qy         69 YKSSIDLYFYVIGSSYENELMLMAVLNCLFDSLSQMLRKNVEKRALLENMEGLFLAVDEI 128
              ||   ||:|:| |   ||||:| :||  |||::: :|| ||:||  |:|:: :||: |||
Db         67 YKFVQDLHFFVTGGEEENELILASVLEGLFDAVTLLLRSNVDKREALDNLDLIFLSFDEI 126

Qy        129 VDGGVILESDPQQVVHRVALRGED--VPLTEQ 158
              :|||::||:|   :  :  :   |   ||:||
Db        127 IDGGIVLETDANVIAGKAGINSTDPNAPLSEQ 158


RESULT 4
S52521
coatomer protein zeta chain - yeast (Saccharomyces cerevisiae)
N;Alternate names: protein LPA7w; protein YP8132.03; protein YPL010w; zeta-COP
C;Species: Saccharomyces cerevisiae
C;Date: 08-May-1995 #sequence_revision 21-Jul-1995 #text_change 09-Jul-2004
C;Accession: S52521; S59683; JC5152
R;Badcock, K.; Churcher, C.
submitted to the EMBL Data Library, February 1995
A;Reference number: S52519
A;Accession: S52521
A;Molecule type: DNA
A;Residues: 1-189 <BAD>
A;Cross-references: UNIPROT:P53600; UNIPARC:UPI000005319F; EMBL:Z48483; NID:g683777; PIDN:CAA88376.1; PID:g683780; MIPS:YPL010w
```

SCORE Search Results Details for Application 09556178 and Search Result 20101214_103254_us-09-556-178-5.rup.

This page gives you Search Results detail for the Application 09556178 and Search Result 20101214_103254_us-09-556-178-5.rup.

Go Back to previous page

GenCore version 6.3

OM protein - protein search, using sw model

Run on: December 14, 2010, 11:23:42 ; Search time 96 Seconds
(without alignments)
7637.199 Million cell updates/sec

Title: US-09-556-178-5
Perfect score: 882
Sequence: 1 MEALILEPSLYTVKAILILD.....QTVSQVLQSAKEQIKWSLLR 177

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 12869322 seqs, 4158259533 residues

Total number of hits satisfying chosen parameters: 12869322

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_201011:*
1: uniprot_sprot:*
2: uniprot_trembl:*
SUMMARIES
%

Result No.	Score	Query Match	Length	DB	ID	Description
1	882	100.0	177	1	COPZ1_HUMAN	P61923 RecName: Fu
2	882	100.0	177	1	COPZ1_MOUSE	P61924 RecName: Fu
3	882	100.0	177	1	COPZ1_PONAB	Q5r5f2 RecName: Fu
4	882	100.0	177	2	D4A8T3_RAT	D4a8t3 SubName: Fu
5	882	100.0	177	2	Q542M2_MOUSE	Q542m2 SubName: Fu
6	878	99.5	177	1	COPZ1_BOVIN	P35604 RecName: Fu
7	877	99.4	177	2	Q53FU3_HUMAN	Q53fu3 SubName: Fu
8	847	96.0	177	2	Q28HL1_XENTR	Q28hl1 SubName: Fu
9	846	95.9	177	2	A0AUT9_XENLA	A0aut9 SubName: Fu
10	846	95.9	187	2	Q801P3_XENLA	Q801p3 SubName: Fu
11	845	95.8	177	2	Q9IB48_DANRE	Q9ib48 SubName: Fu
12	843	95.6	177	2	Q6GQG0_XENLA	Q6gqg0 SubName: Fu
13	842	95.5	177	2	Q7SXH1_DANRE	Q7sxh1 SubName: Fu
14	836	94.8	177	2	C3KJY4_ANOFI	C3kjy4 SubName: Fu
15	832	94.3	177	2	B5X5K5_SALSA	B5x5k5 SubName: Fu

16	832	94.3	179	2	C1BY80_ESOLU	C1by80 SubName: Fu
17	828	93.9	177	2	B5X8E4_SALSA	B5x8e4 SubName: Fu
18	828	93.9	177	2	C1BHI5_ONCMY	C1bhi5 SubName: Fu
19	828	93.9	177	2	C3KJ46_ANOFI	C3kj46 SubName: Fu
20	825	93.5	177	2	B9EM01_SALSA	B9em01 SubName: Fu
21	819	92.9	175	2	C1BFE7_ONCMY	C1bfe7 SubName: Fu
22	815	92.4	174	2	B5X954_SALSA	B5x954 SubName: Fu
23	814	92.3	177	2	C1BH82_ONCMY	C1bh82 SubName: Fu
24	813	92.2	163	2	Q8R3M1_MOUSE	Q8r3m1 SubName: Fu
25	810	91.8	177	2	B5XDE2_SALSA	B5xde2 SubName: Fu
26	745.5	84.5	154	2	B4DDX8_HUMAN	B4ddx8 SubName: Fu
27	701.5	79.5	173	2	Q9IB47_DANRE	Q9ib47 SubName: Fu
28	692	78.5	189	2	Q6DKF5_DANRE	Q6dkf5 SubName: Fu
29	683.5	77.5	229	2	C3XTB6_BRAFL	C3xtb6 SubName: Fu
30	673.5	76.4	178	2	B9EQ95_SALSA	B9eq95 SubName: Fu
31	673	76.3	179	2	B9EPB0_SALSA	B9epb0 SubName: Fu
32	673	76.3	210	1	COPZ2_HUMAN	Q9p299 RecName: Fu
33	667	75.6	205	1	COPZ2_MOUSE	Q9jhh9 RecName: Fu
34	666.5	75.6	178	2	C1BHL1_ONCMY	C1bhl1 SubName: Fu
35	664	75.3	203	2	C1BFJ5_ONCMY	C1bfj5 SubName: Fu
36	663	75.2	185	2	Q9CTG7_MOUSE	Q9ctg7 SubName: Fu
37	649	73.6	156	2	Q6P383_XENTR	Q6p383 SubName: Fu
38	625.5	70.9	178	2	E0VA85_PEDHC	E0va85 SubName: Fu
39	623	70.6	183	2	A7S1D0_NEMVE	A7s1d0 SubName: Fu
40	621.5	70.5	177	2	Q16K41_AEDAE	Q16k41 SubName: Fu
41	620.5	70.4	177	2	B0W863_CULQU	B0w863 SubName: Fu
42	620.5	70.4	182	2	D6WPS8_TRICA	D6wps8 SubName: Fu
43	620	70.3	181	2	Q16K40_AEDAE	Q16k40 SubName: Fu
44	619.5	70.2	178	2	C4WUX3_ACYPI	C4wux3 SubName: Fu
45	612.5	69.4	177	2	Q7Q5C2_ANOGA	Q7q5c2 SubName: Fu

ALIGNMENTS

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RESULT 1
COPZ1_HUMAN
ID   COPZ1_HUMAN             Reviewed;         177 AA.
AC   P61923; Q549N6; Q9Y3C3;
DT   07-JUN-2004, integrated into UniProtKB/Swiss-Prot.
DT   07-JUN-2004, sequence version 1.
DT   05-OCT-2010, entry version 66.
DE   RecName: Full=Coatomer subunit zeta-1;
DE   AltName: Full=Zeta-1-coat protein;
DE            Short=Zeta-1 COP;
GN   Name=COPZ1; Synonyms=COPZ; ORFNames=CGI-120, HSPC181;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
OC   Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [MRNA].
RX   MEDLINE=20512057; PubMed=11056392;
RA   Futatsumori M., Kasai K., Takatsu H., Shin H.-W., Nakayama K.;
RT   "Identification and characterization of novel isoforms of COP I
RT   subunits.";
RL   J. Biochem. 128:793-801(2000).
RN   [2]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RX   MEDLINE=20272150; PubMed=10810093; DOI=10.1101/gr.10.5.703;
RA   Lai C.-H., Chou C.-Y., Ch'ang L.-Y., Liu C.-S., Lin W.-C.;
RT   "Identification of novel human genes evolutionarily conserved in
RT   Caenorhabditis elegans by comparative proteomics.";
RL   Genome Res. 10:703-713(2000).
RN   [3]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
```

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RC   TISSUE=Umbilical cord blood;
RX   MEDLINE=20499367; PubMed=11042152; DOI=10.1101/gr.140200;
RA   Zhang Q.-H., Ye M., Wu X.-Y., Ren S.-X., Zhao M., Zhao C.-J., Fu G.,
RA   Shen Y., Fan H.-Y., Lu G., Zhong M., Xu X.-R., Han Z.-G., Zhang J.-W.,
RA   Tao J., Huang Q.-H., Zhou J., Hu G.-X., Gu J., Chen S.-J., Chen Z.;
RT   "Cloning and functional analysis of cDNAs with open reading frames for
RT   300 previously undefined genes expressed in CD34+ hematopoietic
RT   stem/progenitor cells.";
RL   Genome Res. 10:1546-1560(2000).
RN   [4]
RP   NUCLEOTIDE SEQUENCE [MRNA].
RA   Tu Q., Yu L., Hu P.R., Zhang H.L., Huang J., Zhao S.Y.;
RT   "Cloning and expression of a new human cDNA homology to B.taurus z-cop
RT   mRNA.";
RL   Submitted (JUL-2003) to the EMBL/GenBank/DDBJ databases.
RN   [5]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RA   Mural R.J., Istrail S., Sutton G.G., Florea L., Halpern A.L.,
RA   Mobarry C.M., Lippert R., Walenz B., Shatkay H., Dew I., Miller J.R.,
RA   Flanigan M.J., Edwards N.J., Bolanos R., Fasulo D., Halldorsson B.V.,
RA   Hannenhalli S., Turner R., Yooseph S., Lu F., Nusskern D.R.,
RA   Shue B.C., Zheng X.H., Zhong F., Delcher A.L., Huson D.H.,
RA   Kravitz S.A., Mouchard L., Reinert K., Remington K.A., Clark A.G.,
RA   Waterman M.S., Eichler E.E., Adams M.D., Hunkapiller M.W., Myers E.W.,
RA   Venter J.C.;
RL   Submitted (JUL-2005) to the EMBL/GenBank/DDBJ databases.
RN   [6]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC   TISSUE=Placenta;
RX   PubMed=15489334; DOI=10.1101/gr.2596504;
RG   The MGC Project Team;
RT   "The status, quality, and expansion of the NIH full-length cDNA
RT   project: the Mammalian Gene Collection (MGC).";
RL   Genome Res. 14:2121-2127(2004).
RN   [7]
RP   PROTEIN SEQUENCE OF 1-14, ACETYLATION AT MET-1, AND MASS SPECTROMETRY.
RC   TISSUE=Colon carcinoma;
RA   Bienvenut W.V., Zebisch A., Kolch W.;
RL   Submitted (DEC-2008) to UniProtKB.
RN   [8]
RP   PHOSPHORYLATION [LARGE SCALE ANALYSIS] AT SER-161, AND MASS
RP   SPECTROMETRY.
RC   TISSUE=Embryonic kidney;
RX   PubMed=17525332; DOI=10.1126/science.1140321;
RA   Matsuoka S., Ballif B.A., Smogorzewska A., McDonald E.R. III,
RA   Hurov K.E., Luo J., Bakalarski C.E., Zhao Z., Solimini N.,
RA   Lerenthal Y., Shiloh Y., Gygi S.P., Elledge S.J.;
RT   "ATM and ATR substrate analysis reveals extensive protein networks
RT   responsive to DNA damage.";
RL   Science 316:1160-1166(2007).
RN   [9]
RP   IDENTIFICATION BY MASS SPECTROMETRY [LARGE SCALE ANALYSIS].
RA   Colinge J., Superti-Furga G., Bennett K.L.;
RL   Submitted (OCT-2008) to UniProtKB.
RN   [10]
RP   ACETYLATION [LARGE SCALE ANALYSIS] AT MET-1, AND MASS SPECTROMETRY.
RC   TISSUE=Embryonic kidney;
RX   PubMed=19413330; DOI=10.1021/ac9004309;
RA   Gauci S., Helbig A.O., Slijper M., Krijgsveld J., Heck A.J.,
RA   Mohammed S.;
RT   "Lys-N and trypsin cover complementary parts of the phosphoproteome in
RT   a refined SCX-based approach.";
RL   Anal. Chem. 81:4493-4501(2009).
RN   [11]
RP   STRUCTURE BY NMR.
RA   Yu W., Jin C., Xia B.;
RT   "The NMR structure of human zeta-COP.";
```

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RL   Submitted (JUN-2007) to the PDB data bank.
CC   -!- FUNCTION: The coatomer is a cytosolic protein complex that binds
CC       to dilysine motifs and reversibly associates with Golgi non-
CC       clathrin-coated vesicles, which further mediate biosynthetic
CC       protein transport from the ER, via the Golgi up to the trans Golgi
CC       network. Coatomer complex is required for budding from Golgi
CC       membranes, and is essential for the retrograde Golgi-to-ER
CC       transport of dilysine-tagged proteins. In mammals, the coatomer
CC       can only be recruited by membranes associated to ADP-ribosylation
CC       factors (ARFs), which are small GTP-binding proteins; the complex
CC       also influences the Golgi structural integrity, as well as the
CC       processing, activity, and endocytic recycling of LDL receptors (By
CC       similarity).
CC   -!- FUNCTION: The zeta subunit may be involved in regulating the coat
CC       assembly and, hence, the rate of biosynthetic protein transport
CC       due to its association-dissociation properties with the coatomer
CC       complex.
CC   -!- SUBUNIT: Oligomeric complex that consists of at least the alpha,
CC       beta, beta', gamma, delta, epsilon and zeta subunits.
CC   -!- SUBCELLULAR LOCATION: Cytoplasm (By similarity). Golgi apparatus
CC       membrane; Peripheral membrane protein; Cytoplasmic side (By
CC       similarity). Cytoplasmic vesicle, COPI-coated vesicle membrane;
CC       Peripheral membrane protein; Cytoplasmic side (By similarity).
CC       Note=The coatomer is cytoplasmic or polymerized on the cytoplasmic
CC       side of the Golgi, as well as on the vesicles/buds originating
CC       from it (By similarity).
CC   -!- PTM: Phosphorylated upon DNA damage, probably by ATM or ATR.
CC   -!- SIMILARITY: Belongs to the adaptor complexes small subunit family.
CC   ---------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---------------------------------------------------------------------
DR   EMBL; AB047848; BAB17659.1; -; mRNA.
DR   EMBL; AF151878; AAD34115.1; -; mRNA.
DR   EMBL; AF161529; AAF29144.1; -; mRNA.
DR   EMBL; AF086911; AAP97141.1; -; mRNA.
DR   EMBL; CH471054; EAW96774.1; -; Genomic_DNA.
DR   EMBL; BC002849; AAH02849.1; -; mRNA.
DR   IPI; IPI00032851; -.
DR   RefSeq; NP_057141.1; -.
DR   UniGene; Hs.505652; -.
DR   PDB; 2HF6; NMR; -; A=1-149.
DR   PDBsum; 2HF6; -.
DR   ProteinModelPortal; P61923; -.
DR   DIP; DIP-29873N; -.
DR   IntAct; P61923; 3.
DR   STRING; P61923; -.
DR   PhosphoSite; P61923; -.
DR   PRIDE; P61923; -.
DR   Ensembl; ENST00000262061; ENSP00000262061; ENSG00000111481.
DR   GeneID; 22818; -.
DR   KEGG; hsa:22818; -.
DR   UCSC; uc001sfs.1; human.
DR   CTD; 22818; -.
DR   GeneCards; GC12P054718; -.
DR   H-InvDB; HIX0010694; -.
DR   HGNC; HGNC:2243; COPZ1.
DR   PharmGKB; PA26760; -.
DR   eggNOG; prNOG08087; -.
DR   HOGENOM; HBG326766; -.
DR   HOVERGEN; HBG051077; -.
DR   InParanoid; P61923; -.
DR   OMA; YDDTYPT; -.
DR   PhylomeDB; P61923; -.
DR   Reactome; REACT_11123; Membrane Trafficking.
DR   NextBio; 43208; -.
DR   ArrayExpress; P61923; -.
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DR   Bgee; P61923; -.
DR   CleanEx; HS_COPZ1; -.
DR   Genevestigator; P61923; -.
DR   GermOnline; ENSG00000111481; Homo sapiens.
DR   GO; GO:0030126; C:COPI vesicle coat; IDA:UniProtKB.
DR   GO; GO:0005829; C:cytosol; EXP:Reactome.
DR   GO; GO:0005515; F:protein binding; IEA:InterPro.
DR   GO; GO:0048205; P:COPI coating of Golgi vesicle; EXP:Reactome.
DR   GO; GO:0006891; P:intra-Golgi vesicle-mediated transport; IDA:UniProtKB.
DR   GO; GO:0006886; P:intracellular protein transport; IEA:InterPro.
DR   GO; GO:0006890; P:retrograde vesicle-mediated transport, Golg. . .; TAS:UniProtKB.
DR   InterPro; IPR022775; AP_mu_sigma_su.
DR   InterPro; IPR000804; Clathrin_sm-chain_CS.
DR   InterPro; IPR011012; Longin-like.
DR   Pfam; PF01217; Clat_adaptor_s; 1.
DR   SUPFAM; SSF64356; Longin_like; 1.
DR   PROSITE; PS00989; CLAT_ADAPTOR_S; 1.
PE   1: Evidence at protein level;
KW   3D-structure; Acetylation; Complete proteome; Cytoplasm;
KW   Cytoplasmic vesicle; Direct protein sequencing; ER-Golgi transport;
KW   Golgi apparatus; Membrane; Phosphoprotein; Protein transport;
KW   Transport.
FT   CHAIN         1    177       Coatomer subunit zeta-1.
FT                                /FTId=PRO_0000193825.
FT   MOD_RES       1      1       N-acetylmethionine.
FT   MOD_RES     161    161       Phosphoserine.
FT   STRAND       14     20
FT   STRAND       25     30
FT   HELIX        38     52
FT   STRAND       59     62
FT   STRAND       65     72
FT   STRAND       75     81
FT   HELIX        88    105
FT   HELIX       111    115
FT   HELIX       118    128
FT   HELIX       139    148

  Query Match             100.0%;  Score 882;  DB 1;  Length 177;
  Best Local Similarity   100.0%;
  Matches  177;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MEALILEPSLYTVKAILILDNDGDRLFAKYYDDTYPSVKEQKAFEKNIFNKTHRTDSEIA 60
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Db          1 MEALILEPSLYTVKAILILDNDGDRLFAKYYDDTYPSVKEQKAFEKNIFNKTHRTDSEIA 60

Qy         61 LLEGLTVVYKSSIDLYFYVIGSSYENELMLMAVLNCLFDSLSQMLRKNVEKRALLENMEG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LLEGLTVVYKSSIDLYFYVIGSSYENELMLMAVLNCLFDSLSQMLRKNVEKRALLENMEG 120

Qy        121 LFLAVDEIVDGGVILESDPQQVVHRVALRGEDVPLTEQTVSQVLQSAKEQIKWSLLR 177
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 LFLAVDEIVDGGVILESDPQQVVHRVALRGEDVPLTEQTVSQVLQSAKEQIKWSLLR 177


RESULT 2
COPZ1_MOUSE
ID   COPZ1_MOUSE             Reviewed;         177 AA.
AC   P61924; Q9Y3C3;
DT   07-JUN-2004, integrated into UniProtKB/Swiss-Prot.
DT   07-JUN-2004, sequence version 1.
DT   05-OCT-2010, entry version 58.
DE   RecName: Full=Coatomer subunit zeta-1;
DE   AltName: Full=Zeta-1-coat protein;
DE            Short=Zeta-1 COP;
GN   Name=Copz1; Synonyms=Copz;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muroidea; Muridae; Murinae; Mus; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [MRNA].
RA   Hahn Y., Chung J.H.;
RT   "Murine Copz1 gene encoding nonclathrin coat protein zeta-COP.";
RL   Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC   STRAIN=C57BL/6J;
RX   PubMed=16141072; DOI=10.1126/science.1112014;
RA   Carninci P., Kasukawa T., Katayama S., Gough J., Frith M.C., Maeda N.,
RA   Oyama R., Ravasi T., Lenhard B., Wells C., Kodzius R., Shimokawa K.,
RA   Bajic V.B., Brenner S.E., Batalov S., Forrest A.R., Zavolan M.,
RA   Davis M.J., Wilming L.G., Aidinis V., Allen J.E.,
RA   Ambesi-Impiombato A., Apweiler R., Aturaliya R.N., Bailey T.L.,
RA   Bansal M., Baxter L., Beisel K.W., Bersano T., Bono H., Chalk A.M.,
RA   Chiu K.P., Choudhary V., Christoffels A., Clutterbuck D.R.,
RA   Crowe M.L., Dalla E., Dalrymple B.P., de Bono B., Della Gatta G.,
RA   di Bernardo D., Down T., Engstrom P., Fagiolini M., Faulkner G.,
RA   Fletcher C.F., Fukushima T., Furuno M., Futaki S., Gariboldi M.,
RA   Georgii-Hemming P., Gingeras T.R., Gojobori T., Green R.E.,
RA   Gustincich S., Harbers M., Hayashi Y., Hensch T.K., Hirokawa N.,
RA   Hill D., Huminiecki L., Iacono M., Ikeo K., Iwama A., Ishikawa T.,
RA   Jakt M., Kanapin A., Katoh M., Kawasawa Y., Kelso J., Kitamura H.,
RA   Kitano H., Kollias G., Krishnan S.P., Kruger A., Kummerfeld S.K.,
RA   Kurochkin I.V., Lareau L.F., Lazarevic D., Lipovich L., Liu J.,
RA   Liuni S., McWilliam S., Madan Babu M., Madera M., Marchionni L.,
RA   Matsuda H., Matsuzawa S., Miki H., Mignone F., Miyake S., Morris K.,
RA   Mottagui-Tabar S., Mulder N., Nakano N., Nakauchi H., Ng P.,
RA   Nilsson R., Nishiguchi S., Nishikawa S., Nori F., Ohara O.,
RA   Okazaki Y., Orlando V., Pang K.C., Pavan W.J., Pavesi G., Pesole G.,
RA   Petrovsky N., Piazza S., Reed J., Reid J.F., Ring B.Z., Ringwald M.,
RA   Rost B., Ruan Y., Salzberg S.L., Sandelin A., Schneider C.,
RA   Schoenbach C., Sekiguchi K., Semple C.A., Seno S., Sessa L., Sheng Y.,
RA   Shibata Y., Shimada H., Shimada K., Silva D., Sinclair B.,
RA   Sperling S., Stupka E., Sugiura K., Sultana R., Takenaka Y., Taki K.,
RA   Tammoja K., Tan S.L., Tang S., Taylor M.S., Tegner J., Teichmann S.A.,
RA   Ueda H.R., van Nimwegen E., Verardo R., Wei C.L., Yagi K.,
RA   Yamanishi H., Zabarovsky E., Zhu S., Zimmer A., Hide W., Bult C.,
RA   Grimmond S.M., Teasdale R.D., Liu E.T., Brusic V., Quackenbush J.,
RA   Wahlestedt C., Mattick J.S., Hume D.A., Kai C., Sasaki D., Tomaru Y.,
RA   Fukuda S., Kanamori-Katayama M., Suzuki M., Aoki J., Arakawa T.,
RA   Iida J., Imamura K., Itoh M., Kato T., Kawaji H., Kawagashira N.,
RA   Kawashima T., Kojima M., Kondo S., Konno H., Nakano K., Ninomiya N.,
RA   Nishio T., Okada M., Plessy C., Shibata K., Shiraki T., Suzuki S.,
RA   Tagami M., Waki K., Watahiki A., Okamura-Oho Y., Suzuki H., Kawai J.,
RA   Hayashizaki Y.;
RT   "The transcriptional landscape of the mammalian genome.";
RL   Science 309:1559-1563(2005).
RN   [3]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC   STRAIN=C57BL/6, and C57BL/6J; TISSUE=Brain, and Embryo;
RX   PubMed=15489334; DOI=10.1101/gr.2596504;
RG   The MGC Project Team;
RT   "The status, quality, and expansion of the NIH full-length cDNA
RT   project: the Mammalian Gene Collection (MGC).";
RL   Genome Res. 14:2121-2127(2004).
CC   -!- FUNCTION: The coatomer is a cytosolic protein complex that binds
CC       to dilysine motifs and reversibly associates with Golgi non-
CC       clathrin-coated vesicles, which further mediate biosynthetic
CC       protein transport from the ER, via the Golgi up to the trans Golgi
CC       network. Coatomer complex is required for budding from Golgi
CC       membranes, and is essential for the retrograde Golgi-to-ER
CC       transport of dilysine-tagged proteins. In mammals, the coatomer
CC       can only be recruited by membranes associated to ADP-ribosylation
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CC       factors (ARFs), which are small GTP-binding proteins; the complex
CC       also influences the Golgi structural integrity, as well as the
CC       processing, activity, and endocytic recycling of LDL receptors (By
CC       similarity).
CC   -!- FUNCTION: The zeta subunit may be involved in regulating the coat
CC       assembly and, hence, the rate of biosynthetic protein transport
CC       due to its association-dissociation properties with the coatomer
CC       complex (By similarity).
CC   -!- SUBUNIT: Oligomeric complex that consists of at least the alpha,
CC       beta, beta', gamma, delta, epsilon and zeta subunits (By
CC       similarity).
CC   -!- SUBCELLULAR LOCATION: Cytoplasm (By similarity). Golgi apparatus
CC       membrane; Peripheral membrane protein; Cytoplasmic side (By
CC       similarity). Cytoplasmic vesicle, COPI-coated vesicle membrane;
CC       Peripheral membrane protein; Cytoplasmic side (By similarity).
CC       Note=The coatomer is cytoplasmic or polymerized on the cytoplasmic
CC       side of the Golgi, as well as on the vesicles/buds originating
CC       from it (By similarity).
CC   -!- PTM: Phosphorylated upon DNA damage, probably by ATM or ATR (By
CC       similarity).
CC   -!- SIMILARITY: Belongs to the adaptor complexes small subunit family.
CC   ---------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---------------------------------------------------------------------
DR   EMBL; AB037370; BAA90303.1; -; mRNA.
DR   EMBL; AK003302; BAB22703.1; -; mRNA.
DR   EMBL; BC002246; -; NOT_ANNOTATED_CDS; mRNA.
DR   EMBL; BC058524; AAH58524.1; -; mRNA.
DR   EMBL; BC085314; AAH85314.1; -; mRNA.
DR   IPI; IPI00139637; -.
DR   RefSeq; NP_062791.1; -.
DR   UniGene; Mm.29473; -.
DR   ProteinModelPortal; P61924; -.
DR   SMR; P61924; 1-149.
DR   STRING; P61924; -.
DR   PhosphoSite; P61924; -.
DR   PRIDE; P61924; -.
DR   Ensembl; ENSMUST00000100162; ENSMUSP00000097738; ENSMUSG00000060992.
DR   GeneID; 56447; -.
DR   KEGG; mmu:56447; -.
DR   UCSC; uc007xxv.1; mouse.
DR   CTD; 56447; -.
DR   MGI; MGI:1929063; Copz1.
DR   eggNOG; roNOG15155; -.
DR   HOGENOM; HBG326766; -.
DR   HOVERGEN; HBG051077; -.
DR   InParanoid; P61924; -.
DR   OMA; YDDTYPT; -.
DR   PhylomeDB; P61924; -.
DR   NextBio; 312654; -.
DR   ArrayExpress; P61924; -.
DR   Bgee; P61924; -.
DR   CleanEx; MM_COPZ1; -.
DR   Genevestigator; P61924; -.
DR   GermOnline; ENSMUSG00000060992; Mus musculus.
DR   GO; GO:0030126; C:COPI vesicle coat; ISS:UniProtKB.
DR   GO; GO:0005515; F:protein binding; IEA:InterPro.
DR   GO; GO:0006891; P:intra-Golgi vesicle-mediated transport; ISS:UniProtKB.
DR   GO; GO:0006886; P:intracellular protein transport; IEA:InterPro.
DR   InterPro; IPR022775; AP_mu_sigma_su.
DR   InterPro; IPR000804; Clathrin_sm-chain_CS.
DR   InterPro; IPR011012; Longin-like.
DR   Pfam; PF01217; Clat_adaptor_s; 1.
DR   SUPFAM; SSF64356; Longin_like; 1.
DR   PROSITE; PS00989; CLAT_ADAPTOR_S; 1.
PE   2: Evidence at transcript level;
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KW   Acetylation; Cytoplasm; Cytoplasmic vesicle; ER-Golgi transport;
KW   Golgi apparatus; Membrane; Phosphoprotein; Protein transport;
KW   Transport.
FT   CHAIN         1    177       Coatomer subunit zeta-1.
FT                                /FTId=PRO_0000193826.
FT   MOD_RES       1      1       N-acetylmethionine (By similarity).
FT   MOD_RES     161    161       Phosphoserine (By similarity).
SQ   SEQUENCE   177 AA;  20198 MW;  355530D032D3A049 CRC64;

  Query Match             100.0%;  Score 882;  DB 1;  Length 177;
  Best Local Similarity   100.0%;
  Matches  177;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MEALILEPSLYTVKAILILDNDGDRLFAKYYDDTYPSVKEQKAFEKNIFNKTHRTDSEIA 60
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Db          1 MEALILEPSLYTVKAILILDNDGDRLFAKYYDDTYPSVKEQKAFEKNIFNKTHRTDSEIA 60

Qy         61 LLEGLTVVYKSSIDLYFYVIGSSYENELMLMAVLNCLFDSLSQMLRKNVEKRALLENMEG 120
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Db         61 LLEGLTVVYKSSIDLYFYVIGSSYENELMLMAVLNCLFDSLSQMLRKNVEKRALLENMEG 120

Qy        121 LFLAVDEIVDGGVILESDPQQVVHRVALRGEDVPLTEQTVSQVLQSAKEQIKWSLLR 177
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Db        121 LFLAVDEIVDGGVILESDPQQVVHRVALRGEDVPLTEQTVSQVLQSAKEQIKWSLLR 177


RESULT 3
COPZ1_PONAB
ID   COPZ1_PONAB             Reviewed;         177 AA.
AC   Q5R5F2;
DT   13-SEP-2005, integrated into UniProtKB/Swiss-Prot.
DT   21-DEC-2004, sequence version 1.
DT   05-OCT-2010, entry version 37.
DE   RecName: Full=Coatomer subunit zeta-1;
DE   AltName: Full=Zeta-1-coat protein;
DE            Short=Zeta-1 COP;
GN   Name=COPZ1; Synonyms=COPZ;
OS   Pongo abelii (Sumatran orangutan).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
OC   Catarrhini; Hominidae; Pongo.
OX   NCBI_TaxID=9601;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC   TISSUE=Kidney;
RG   The German cDNA consortium;
RL   Submitted (NOV-2004) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: The coatomer is a cytosolic protein complex that binds
CC       to dilysine motifs and reversibly associates with Golgi non-
CC       clathrin-coated vesicles, which further mediate biosynthetic
CC       protein transport from the ER, via the Golgi up to the trans Golgi
CC       network. Coatomer complex is required for budding from Golgi
CC       membranes, and is essential for the retrograde Golgi-to-ER
CC       transport of dilysine-tagged proteins. In mammals, the coatomer
CC       can only be recruited by membranes associated to ADP-ribosylation
CC       factors (ARFs), which are small GTP-binding proteins; the complex
CC       also influences the Golgi structural integrity, as well as the
CC       processing, activity, and endocytic recycling of LDL receptors (By
CC       similarity).
CC   -!- FUNCTION: The zeta subunit may be involved in regulating the coat
CC       assembly and, hence, the rate of biosynthetic protein transport
CC       due to its association-dissociation properties with the coatomer
CC       complex (By similarity).
CC   -!- SUBUNIT: Oligomeric complex that consists of at least the alpha,
CC       beta, beta', gamma, delta, epsilon and zeta subunits (By
CC       similarity).
CC   -!- SUBCELLULAR LOCATION: Cytoplasm (By similarity). Golgi apparatus
```

```
CC       membrane; Peripheral membrane protein; Cytoplasmic side (By
CC       similarity). Cytoplasmic vesicle, COPI-coated vesicle membrane;
CC       Peripheral membrane protein; Cytoplasmic side (By similarity).
CC       Note=The coatomer is cytoplasmic or polymerized on the cytoplasmic
CC       side of the Golgi, as well as on the vesicles/buds originating
CC       from it (By similarity).
CC   -!- PTM: Phosphorylated upon DNA damage, probably by ATM or ATR (By
CC       similarity).
CC   -!- SIMILARITY: Belongs to the adaptor complexes small subunit family.
CC   ---------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---------------------------------------------------------------------
DR   EMBL; CR860909; CAH93014.1; -; mRNA.
DR   RefSeq; NP_001127620.1; -.
DR   UniGene; Pab.18608; -.
DR   ProteinModelPortal; Q5R5F2; -.
DR   SMR; Q5R5F2; 1-149.
DR   GeneID; 100174699; -.
DR   CTD; 100174699; -.
DR   HOVERGEN; HBG051077; -.
DR   InParanoid; Q5R5F2; -.
DR   OMA; YDDTYPT; -.
DR   OrthoDB; EOG969TD6; -.
DR   GO; GO:0030126; C:COPI vesicle coat; ISS:UniProtKB.
DR   GO; GO:0005515; F:protein binding; IEA:InterPro.
DR   GO; GO:0006891; P:intra-Golgi vesicle-mediated transport; ISS:UniProtKB.
DR   GO; GO:0006886; P:intracellular protein transport; IEA:InterPro.
DR   InterPro; IPR022775; AP_mu_sigma_su.
DR   InterPro; IPR000804; Clathrin_sm-chain_CS.
DR   InterPro; IPR011012; Longin-like.
DR   Pfam; PF01217; Clat_adaptor_s; 1.
DR   SUPFAM; SSF64356; Longin_like; 1.
DR   PROSITE; PS00989; CLAT_ADAPTOR_S; 1.
PE   2: Evidence at transcript level;
KW   Acetylation; Cytoplasm; Cytoplasmic vesicle; ER-Golgi transport;
KW   Golgi apparatus; Membrane; Phosphoprotein; Protein transport;
KW   Transport.
FT   CHAIN         1    177       Coatomer subunit zeta-1.
FT                                /FTId=PRO_0000193827.
FT   MOD_RES       1      1       N-acetylmethionine (By similarity).
FT   MOD_RES     161    161       Phosphoserine (By similarity).
SQ   SEQUENCE   177 AA;  20198 MW;  355530D032D3A049 CRC64;

  Query Match             100.0%;  Score 882;  DB 1;  Length 177;
  Best Local Similarity   100.0%;
  Matches  177;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MEALILEPSLYTVKAILILDNDGDRLFAKYYDDTYPSVKEQKAFEKNIFNKTHRTDSEIA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MEALILEPSLYTVKAILILDNDGDRLFAKYYDDTYPSVKEQKAFEKNIFNKTHRTDSEIA 60

Qy         61 LLEGLTVVYKSSIDLYFYVIGSSYENELMLMAVLNCLFDSLSQMLRKNVEKRALLENMEG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LLEGLTVVYKSSIDLYFYVIGSSYENELMLMAVLNCLFDSLSQMLRKNVEKRALLENMEG 120

Qy        121 LFLAVDEIVDGGVILESDPQQVVHRVALRGEDVPLTEQTVSQVLQSAKEQIKWSLLR 177
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Db        121 LFLAVDEIVDGGVILESDPQQVVHRVALRGEDVPLTEQTVSQVLQSAKEQIKWSLLR 177


RESULT 4
D4A8T3_RAT
ID   D4A8T3_RAT              Unreviewed;       177 AA.
AC   D4A8T3;
DT   20-APR-2010, integrated into UniProtKB/TrEMBL.
DT   20-APR-2010, sequence version 1.
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DT   02-NOV-2010, entry version 7.
DE   SubName: Full=Coatomer protein complex, subunit zeta 1 (Predicted);
DE   SubName: Full=Uncharacterized protein;
GN   Name=Copz1; Synonyms=Copz1_predicted; ORFNames=rCG_50578;
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muroidea; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   IDENTIFICATION.
RG   Ensembl;
RL   Submitted (MAR-2010) to UniProtKB.
RN   [2]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC   STRAIN=Brown Norway;
RX   PubMed=15057822; DOI=10.1038/nature02426;
RA   Gibbs R.A., Weinstock G.M., Metzker M.L., Muzny D.M., Sodergren E.J.,
RA   Scherer S., Scott G., Steffen D., Worley K.C., Burch P.E., Okwuonu G.,
RA   Hines S., Lewis L., Deramo C., Delgado O., Dugan-Rocha S., Miner G.,
RA   Morgan M., Hawes A., Gill R., Holt R.A., Adams M.D., Amanatides P.G.,
RA   Baden-Tillson H., Barnstead M., Chin S., Evans C.A., Ferriera S.,
RA   Fosler C., Glodek A., Gu Z., Jennings D., Kraft C.L., Nguyen T.,
RA   Pfannkoch C.M., Sitter C., Sutton G.G., Venter J.C., Woodage T.,
RA   Smith D., Lee H.-M., Gustafson E., Cahill P., Kana A.,
RA   Doucette-Stamm L., Weinstock K., Fechtel K., Weiss R.B., Dunn D.M.,
RA   Green E.D., Blakesley R.W., Bouffard G.G., De Jong P.J., Osoegawa K.,
RA   Zhu B., Marra M., Schein J., Bosdet I., Fjell C., Jones S.,
RA   Krzywinski M., Mathewson C., Siddiqui A., Wye N., McPherson J.,
RA   Zhao S., Fraser C.M., Shetty J., Shatsman S., Geer K., Chen Y.,
RA   Abramzon S., Nierman W.C., Havlak P.H., Chen R., Durbin K.J., Egan A.,
RA   Ren Y., Song X.-Z., Li B., Liu Y., Qin X., Cawley S., Cooney A.J.,
RA   D'Souza L.M., Martin K., Wu J.Q., Gonzalez-Garay M.L., Jackson A.R.,
RA   Kalafus K.J., McLeod M.P., Milosavljevic A., Virk D., Volkov A.,
RA   Wheeler D.A., Zhang Z., Bailey J.A., Eichler E.E., Tuzun E.,
RA   Birney E., Mongin E., Ureta-Vidal A., Woodwark C., Zdobnov E.,
RA   Bork P., Suyama M., Torrents D., Alexandersson M., Trask B.J.,
RA   Young J.M., Huang H., Wang H., Xing H., Daniels S., Gietzen D.,
RA   Schmidt J., Stevens K., Vitt U., Wingrove J., Camara F., Mar Alba M.,
RA   Abril J.F., Guigo R., Smit A., Dubchak I., Rubin E.M., Couronne O.,
RA   Poliakov A., Huebner N., Ganten D., Goesele C., Hummel O.,
RA   Kreitler T., Lee Y.-A., Monti J., Schulz H., Zimdahl H.,
RA   Himmelbauer H., Lehrach H., Jacob H.J., Bromberg S.,
RA   Gullings-Handley J., Jensen-Seaman M.I., Kwitek A.E., Lazar J.,
RA   Pasko D., Tonellato P.J., Twigger S., Ponting C.P., Duarte J.M.,
RA   Rice S., Goodstadt L., Beatson S.A., Emes R.D., Winter E.E.,
RA   Webber C., Brandt P., Nyakatura G., Adetobi M., Chiaromonte F.,
RA   Elnitski L., Eswara P., Hardison R.C., Hou M., Kolbe D., Makova K.,
RA   Miller W., Nekrutenko A., Riemer C., Schwartz S., Taylor J., Yang S.,
RA   Zhang Y., Lindpaintner K., Andrews T.D., Caccamo M., Clamp M.,
RA   Clarke L., Curwen V., Durbin R.M., Eyras E., Searle S.M., Cooper G.M.,
RA   Batzoglou S., Brudno M., Sidow A., Stone E.A., Payseur B.A.,
RA   Bourque G., Lopez-Otin C., Puente X.S., Chakrabarti K., Chatterji S.,
RA   Dewey C., Pachter L., Bray N., Yap V.B., Caspi A., Tesler G.,
RA   Pevzner P.A., Haussler D., Roskin K.M., Baertsch R., Clawson H.,
RA   Furey T.S., Hinrichs A.S., Karolchik D., Kent W.J., Rosenbloom K.R.,
RA   Trumbower H., Weirauch M., Cooper D.N., Stenson P.D., Ma B., Brent M.,
RA   Arumugam M., Shteynberg D., Copley R.R., Taylor M.S., Riethman H.,
RA   Mudunuri U., Peterson J., Guyer M., Felsenfeld A., Old S., Mockrin S.,
RA   Collins F.S.;
RT   "Genome sequence of the Brown Norway rat yields insights into
RT   mammalian evolution.";
RL   Nature 428:493-521(2004).
RN   [3]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=BN;
RX   PubMed=15632090; DOI=10.1101/gr.2889405;
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RA   Florea L., Di Francesco V., Miller J., Turner R., Yao A., Harris M.,
RA   Walenz B., Mobarry C., Merkulov G.V., Charlab R., Dew I., Deng Z.,
RA   Istrail S., Li P., Sutton G.;
RT   "Gene and alternative splicing annotation with AIR.";
RL   Genome Res. 15:54-66(2005).
RN   [4]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=BN;
RA   Mural R.J., Li P.W., Adams M.D., Amanatides P.G., Baden-Tillson H.,
RA   Barnstead M., Chin S.H., Dew I., Evans C.A., Ferriera S., Flanigan M.,
RA   Fosler C., Glodek A., Gu Z., Holt R.A., Jennings D., Kraft C.L.,
RA   Lu F., Nguyen T., Nusskern D.R., Pfannkoch C.M., Sitter C.,
RA   Sutton G.G., Venter J.C., Wang Z., Woodage T., Zheng X.H., Zhong F.;
RL   Submitted (SEP-2005) to the EMBL/GenBank/DDBJ databases.
CC   ---------------------------------------------------------------------
CC   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC   Distributed under the Creative Commons Attribution-NoDerivs License
CC   ---------------------------------------------------------------------
DR   EMBL; CH474035; EDL86787.1; -; Genomic_DNA.
DR   IPI; IPI00949165; -.
DR   RefSeq; NP_001101587.1; -.
DR   UniGene; Rn.159796; -.
DR   ProteinModelPortal; D4A8T3; -.
DR   SMR; D4A8T3; 1-149.
DR   Ensembl; ENSRNOT00000065270; ENSRNOP00000059082; ENSRNOG00000036835.
DR   GeneID; 315345; -.
DR   KEGG; rno:315345; -.
DR   CTD; 315345; -.
DR   RGD; 1306154; Copz1.
DR   GO; GO:0030117; C:membrane coat; IEA:InterPro.
DR   GO; GO:0005515; F:protein binding; IEA:InterPro.
DR   GO; GO:0006886; P:intracellular protein transport; IEA:InterPro.
DR   GO; GO:0016192; P:vesicle-mediated transport; IEA:InterPro.
DR   InterPro; IPR022775; AP_mu_sigma_su.
DR   InterPro; IPR000804; Clathrin_sm-chain_CS.
DR   InterPro; IPR011012; Longin-like.
DR   Pfam; PF01217; Clat_adaptor_s; 1.
DR   SUPFAM; SSF64356; Longin_like; 1.
DR   PROSITE; PS00989; CLAT_ADAPTOR_S; 1.
PE   4: Predicted;
SQ   SEQUENCE   177 AA;  20198 MW;  355530D032D3A049 CRC64;

  Query Match             100.0%;  Score 882;  DB 2;  Length 177;
  Best Local Similarity   100.0%;
  Matches  177;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MEALILEPSLYTVKAILILDNDGDRLFAKYYDDTYPSVKEQKAFEKNIFNKTHRTDSEIA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MEALILEPSLYTVKAILILDNDGDRLFAKYYDDTYPSVKEQKAFEKNIFNKTHRTDSEIA 60

Qy         61 LLEGLTVVYKSSIDLYFYVIGSSYENELMLMAVLNCLFDSLSQMLRKNVEKRALLENMEG 120
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Db         61 LLEGLTVVYKSSIDLYFYVIGSSYENELMLMAVLNCLFDSLSQMLRKNVEKRALLENMEG 120

Qy        121 LFLAVDEIVDGGVILESDPQQVVHRVALRGEDVPLTEQTVSQVLQSAKEQIKWSLLR 177
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Db        121 LFLAVDEIVDGGVILESDPQQVVHRVALRGEDVPLTEQTVSQVLQSAKEQIKWSLLR 177


RESULT 5
Q542M2_MOUSE
ID   Q542M2_MOUSE            Unreviewed;       177 AA.
AC   Q542M2;
DT   24-MAY-2005, integrated into UniProtKB/TrEMBL.
DT   24-MAY-2005, sequence version 1.
DT   05-OCT-2010, entry version 50.
DE   SubName: Full=Coatomer protein complex, subunit zeta 1, isoform CRA_c;
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DE   SubName: Full=Copz1 protein;
DE   SubName: Full=Putative uncharacterized protein;
GN   Name=Copz1; ORFNames=mCG_15682;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muroidea; Muridae; Murinae; Mus; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC   STRAIN=C57BL/6J, and NOD; TISSUE=Spinal ganglion, Amnion, Placenta,
RC   and Activated spleen;
RX   PubMed=16141072; DOI=10.1126/science.1112014;
RA   Carninci P., Kasukawa T., Katayama S., Gough J., Frith M.C., Maeda N.,
RA   Oyama R., Ravasi T., Lenhard B., Wells C., Kodzius R., Shimokawa K.,
RA   Bajic V.B., Brenner S.E., Batalov S., Forrest A.R., Zavolan M.,
RA   Davis M.J., Wilming L.G., Aidinis V., Allen J.E.,
RA   Ambesi-Impiombato A., Apweiler R., Aturaliya R.N., Bailey T.L.,
RA   Bansal M., Baxter L., Beisel K.W., Bersano T., Bono H., Chalk A.M.,
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RA   di Bernardo D., Down T., Engstrom P., Fagiolini M., Faulkner G.,
RA   Fletcher C.F., Fukushima T., Furuno M., Futaki S., Gariboldi M.,
RA   Georgii-Hemming P., Gingeras T.R., Gojobori T., Green R.E.,
RA   Gustincich S., Harbers M., Hayashi Y., Hensch T.K., Hirokawa N.,
RA   Hill D., Huminiecki L., Iacono M., Ikeo K., Iwama A., Ishikawa T.,
RA   Jakt M., Kanapin A., Katoh M., Kawasawa Y., Kelso J., Kitamura H.,
RA   Kitano H., Kollias G., Krishnan S.P., Kruger A., Kummerfeld S.K.,
RA   Kurochkin I.V., Lareau L.F., Lazarevic D., Lipovich L., Liu J.,
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RA   Shibata Y., Shimada H., Shimada K., Silva D., Sinclair B.,
RA   Sperling S., Stupka E., Sugiura K., Sultana R., Takenaka Y., Taki K.,
RA   Tammoja K., Tan S.L., Tang S., Taylor M.S., Tegner J., Teichmann S.A.,
RA   Ueda H.R., van Nimwegen E., Verardo R., Wei C.L., Yagi K.,
RA   Yamanishi H., Zabarovsky E., Zhu S., Zimmer A., Hide W., Bult C.,
RA   Grimmond S.M., Teasdale R.D., Liu E.T., Brusic V., Quackenbush J.,
RA   Wahlestedt C., Mattick J.S., Hume D.A., Kai C., Sasaki D., Tomaru Y.,
RA   Fukuda S., Kanamori-Katayama M., Suzuki M., Aoki J., Arakawa T.,
RA   Iida J., Imamura K., Itoh M., Kato T., Kawaji H., Kawagashira N.,
RA   Kawashima T., Kojima M., Kondo S., Konno H., Nakano K., Ninomiya N.,
RA   Nishio T., Okada M., Plessy C., Shibata K., Shiraki T., Suzuki S.,
RA   Tagami M., Waki K., Watahiki A., Okamura-Oho Y., Suzuki H., Kawai J.,
RA   Hayashizaki Y.;
RT   "The transcriptional landscape of the mammalian genome.";
RL   Science 309:1559-1563(2005).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=Mixed;
RX   MEDLINE=22036378; PubMed=12040188; DOI=10.1126/science.1069193;
RA   Mural R.J., Adams M.D., Myers E.W., Smith H.O., Miklos G.L., Wides R.,
RA   Halpern A., Li P.W., Sutton G.G., Nadeau J., Salzberg S.L., Holt R.A.,
RA   Kodira C.D., Lu F., Chen L., Deng Z., Evangelista C.C., Gan W.,
RA   Heiman T.J., Li J., Li Z., Merkulov G.V., Milshina N.V., Naik A.K.,
RA   Qi R., Shue B.C., Wang A., Wang J., Wang X., Yan X., Ye J.,
RA   Yooseph S., Zhao Q., Zheng L., Zhu S.C., Biddick K., Bolanos R.,
RA   Delcher A.L., Dew I.M., Fasulo D., Flanigan M.J., Huson D.H.,
RA   Kravitz S.A., Miller J.R., Mobarry C.M., Reinert K., Remington K.A.,
RA   Zhang Q., Zheng X.H., Nusskern D.R., Lai Z., Lei Y., Zhong W., Yao A.,
RA   Guan P., Ji R.R., Gu Z., Wang Z.Y., Zhong F., Xiao C., Chiang C.C.,
RA   Yandell M., Wortman J.R., Amanatides P.G., Hladun S.L., Pratts E.C.,
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RA   Johnson J.E., Dodson K.L., Woodford K.J., Evans C.A., Gropman B.,
RA   Rusch D.B., Venter E., Wang M., Smith T.J., Houck J.T., Tompkins D.E.,
RA   Haynes C., Jacob D., Chin S.H., Allen D.R., Dahlke C.E., Sanders R.,
RA   Li K., Liu X., Levitsky A.A., Majoros W.H., Chen Q., Xia A.C.,
RA   Lopez J.R., Donnelly M.T., Newman M.H., Glodek A., Kraft C.L.,
RA   Nodell M., Ali F., An H.J., Baldwin-Pitts D., Beeson K.Y., Cai S.,
RA   Carnes M., Carver A., Caulk P.M., Center A., Chen Y.H., Cheng M.L.,
RA   Coyne M.D., Crowder M., Danaher S., Davenport L.B., Desilets R.,
RA   Dietz S.M., Doup L., Dullaghan P., Ferriera S., Fosler C.R.,
RA   Gire H.C., Gluecksmann A., Gocayne J.D., Gray J., Hart B., Haynes J.,
RA   Hoover J., Howland T., Ibegwam C., Jalali M., Johns D., Kline L.,
RA   Ma D.S., MacCawley S., Magoon A., Mann F., May D., McIntosh T.C.,
RA   Mehta S., Moy L., Moy M.C., Murphy B.J., Murphy S.D., Nelson K.A.,
RA   Nuri Z., Parker K.A., Prudhomme A.C., Puri V.N., Qureshi H.,
RA   Raley J.C., Reardon M.S., Regier M.A., Rogers Y.H., Romblad D.L.,
RA   Schutz J., Scott J.L., Scott R., Sitter C.D., Smallwood M.,
RA   Sprague A.C., Stewart E., Strong R.V., Suh E., Sylvester K.,
RA   Thomas R., Tint N.N., Tsonis C., Wang G., Wang G., Williams M.S.,
RA   Williams S.M., Windsor S.M., Wolfe K., Wu M.M., Zaveri J.,
RA   Chaturvedi K., Gabrielian A.E., Ke Z., Sun J., Subramanian G.,
RA   Venter J.C., Pfannkoch C.M., Barnstead M., Stephenson L.D.;
RT   "A comparison of whole-genome shotgun-derived mouse chromosome 16 and
RT   the human genome.";
RL   Science 296:1661-1671(2002).
RN   [3]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=Mixed;
RA   Mural R.J., Adams M.D., Myers E.W., Smith H.O., Venter J.C.;
RL   Submitted (SEP-2005) to the EMBL/GenBank/DDBJ databases.
RN   [4]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC   STRAIN=Czech II; TISSUE=Mammary tumor metastatized to lung. Tumor
RC   arose spontaneously;
RX   PubMed=15489334; DOI=10.1101/gr.2596504;
RG   The MGC Project Team;
RT   "The status, quality, and expansion of the NIH full-length cDNA
RT   project: the Mammalian Gene Collection (MGC).";
RL   Genome Res. 14:2121-2127(2004).
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CC   ---------------------------------------------------------------------
DR   EMBL; BC110679; AAI10680.1; -; mRNA.
DR   EMBL; AK083824; BAC39030.1; -; mRNA.
DR   EMBL; AK156758; BAE33841.1; -; mRNA.
DR   EMBL; AK167636; BAE39687.1; -; mRNA.
DR   EMBL; AK168382; BAE40310.1; -; mRNA.
DR   EMBL; AK168471; BAE40362.1; -; mRNA.
DR   EMBL; CH466550; EDL03927.1; -; Genomic_DNA.
DR   IPI; IPI00139637; -.
DR   RefSeq; NP_062791.1; -.
DR   UniGene; Mm.29473; -.
DR   ProteinModelPortal; Q542M2; -.
DR   SMR; Q542M2; 1-149.
DR   STRING; Q542M2; -.
DR   PRIDE; Q542M2; -.
DR   Ensembl; ENSMUST00000100162; ENSMUSP00000097738; ENSMUSG00000060992.
DR   GeneID; 56447; -.
DR   KEGG; mmu:56447; -.
DR   CTD; 56447; -.
DR   MGI; MGI:1929063; Copz1.
DR   HOVERGEN; HBG051077; -.
DR   InParanoid; Q542M2; -.
DR   OMA; YDDTYPT; -.
DR   PhylomeDB; Q542M2; -.
DR   NextBio; 312654; -.
DR   ArrayExpress; Q542M2; -.
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DR   Bgee; Q542M2; -.
DR   Genevestigator; Q542M2; -.
DR   GO; GO:0030117; C:membrane coat; IEA:InterPro.
DR   GO; GO:0005515; F:protein binding; IEA:InterPro.
DR   GO; GO:0006886; P:intracellular protein transport; IEA:InterPro.
DR   InterPro; IPR022775; AP_mu_sigma_su.
DR   InterPro; IPR000804; Clathrin_sm-chain_CS.
DR   InterPro; IPR011012; Longin-like.
DR   Pfam; PF01217; Clat_adaptor_s; 1.
DR   SUPFAM; SSF64356; Longin_like; 1.
DR   PROSITE; PS00989; CLAT_ADAPTOR_S; 1.
PE   2: Evidence at transcript level;
SQ   SEQUENCE   177 AA;  20198 MW;  355530D032D3A049 CRC64;

  Query Match             100.0%;  Score 882;  DB 2;  Length 177;
  Best Local Similarity   100.0%;
  Matches  177;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MEALILEPSLYTVKAILILDNDGDRLFAKYYDDTYPSVKEQKAFEKNIFNKTHRTDSEIA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MEALILEPSLYTVKAILILDNDGDRLFAKYYDDTYPSVKEQKAFEKNIFNKTHRTDSEIA 60

Qy         61 LLEGLTVVYKSSIDLYFYVIGSSYENELMLMAVLNCLFDSLSQMLRKNVEKRALLENMEG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LLEGLTVVYKSSIDLYFYVIGSSYENELMLMAVLNCLFDSLSQMLRKNVEKRALLENMEG 120

Qy        121 LFLAVDEIVDGGVILESDPQQVVHRVALRGEDVPLTEQTVSQVLQSAKEQIKWSLLR 177
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 LFLAVDEIVDGGVILESDPQQVVHRVALRGEDVPLTEQTVSQVLQSAKEQIKWSLLR 177


RESULT 6
COPZ1_BOVIN
ID   COPZ1_BOVIN             Reviewed;         177 AA.
AC   P35604; Q5EA44;
DT   01-JUN-1994, integrated into UniProtKB/Swiss-Prot.
DT   27-JUN-2006, sequence version 2.
DT   05-OCT-2010, entry version 74.
DE   RecName: Full=Coatomer subunit zeta-1;
DE   AltName: Full=Zeta-1-coat protein;
DE            Short=Zeta-1 COP;
GN   Name=COPZ1; Synonyms=COPZ;
OS   Bos taurus (Bovine).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC   Pecora; Bovidae; Bovinae; Bos.
OX   NCBI_TaxID=9913;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [MRNA], AND PROTEIN SEQUENCE OF 55-70; 113-129 AND
RP   146-160.
RC   TISSUE=Liver;
RX   MEDLINE=94103328; PubMed=8276893; DOI=10.1083/jcb.123.6.1727;
RA   Kuge O., Hara-Kuge S., Orci L., Ravazzola M., Amherdt M., Tanigawa G.,
RA   Wieland F.T., Rothman J.E.;
RT   "Zeta-COP, a subunit of coatomer, is required for COP-coated vesicle
RT   assembly.";
RL   J. Cell Biol. 123:1727-1734(1993).
RN   [2]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RX   PubMed=16305752; DOI=10.1186/1471-2164-6-166;
RA   Harhay G.P., Sonstegard T.S., Keele J.W., Heaton M.P., Clawson M.L.,
RA   Snelling W.M., Wiedmann R.T., Van Tassell C.P., Smith T.P.L.;
RT   "Characterization of 954 bovine full-CDS cDNA sequences.";
RL   BMC Genomics 6:166-166(2005).
RN   [3]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC   STRAIN=Crossbred X Angus; TISSUE=Ileum;
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RG   NIH - Mammalian Gene Collection (MGC) project;
RL   Submitted (AUG-2005) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: The coatomer is a cytosolic protein complex that binds
CC       to dilysine motifs and reversibly associates with Golgi non-
CC       clathrin-coated vesicles, which further mediate biosynthetic
CC       protein transport from the ER, via the Golgi up to the trans Golgi
CC       network. Coatomer complex is required for budding from Golgi
CC       membranes, and is essential for the retrograde Golgi-to-ER
CC       transport of dilysine-tagged proteins. In mammals, the coatomer
CC       can only be recruited by membranes associated to ADP-ribosylation
CC       factors (ARFs), which are small GTP-binding proteins; the complex
CC       also influences the Golgi structural integrity, as well as the
CC       processing, activity, and endocytic recycling of LDL receptors (By
CC       similarity).
CC   -!- FUNCTION: The zeta subunit may be involved in regulating the coat
CC       assembly and, hence, the rate of biosynthetic protein transport
CC       due to its association-dissociation properties with the coatomer
CC       complex.
CC   -!- SUBUNIT: Oligomeric complex that consists of at least the alpha,
CC       beta, beta', gamma, delta, epsilon and zeta subunits.
CC   -!- SUBCELLULAR LOCATION: Cytoplasm (By similarity). Golgi apparatus
CC       membrane; Peripheral membrane protein; Cytoplasmic side (By
CC       similarity). Cytoplasmic vesicle, COPI-coated vesicle membrane;
CC       Peripheral membrane protein; Cytoplasmic side (By similarity).
CC       Note=The coatomer is cytoplasmic or polymerized on the cytoplasmic
CC       side of the Golgi, as well as on the vesicles/buds originating
CC       from it (By similarity).
CC   -!- PTM: Phosphorylated upon DNA damage, probably by ATM or ATR (By
CC       similarity).
CC   -!- SIMILARITY: Belongs to the adaptor complexes small subunit family.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; X75935; CAA53539.1; -; mRNA.
DR   EMBL; BT020662; AAX08679.1; -; mRNA.
DR   EMBL; BT020725; AAX08742.1; -; mRNA.
DR   EMBL; BC102358; AAI02359.1; -; mRNA.
DR   IPI; IPI00685319; -.
DR   PIR; A49465; A49465.
DR   RefSeq; NP_776707.2; -.
DR   UniGene; Bt.43744; -.
DR   ProteinModelPortal; P35604; -.
DR   SMR; P35604; 1-149.
DR   IntAct; P35604; 2.
DR   STRING; P35604; -.
DR   Ensembl; ENSBTAT00000007088; ENSBTAP00000007088; ENSBTAG00000005384.
DR   GeneID; 281707; -.
DR   KEGG; bta:281707; -.
DR   CTD; 281707; -.
DR   eggNOG; maNOG17869; -.
DR   HOVERGEN; HBG051077; -.
DR   InParanoid; P35604; -.
DR   OMA; YDDTYPT; -.
DR   OrthoDB; EOG969TD6; -.
DR   PhylomeDB; P35604; -.
DR   BioCyc; CATTLE:281707-MONOMER; -.
DR   GO; GO:0030126; C:COPI vesicle coat; IDA:UniProtKB.
DR   GO; GO:0005515; F:protein binding; IEA:InterPro.
DR   GO; GO:0006891; P:intra-Golgi vesicle-mediated transport; IDA:UniProtKB.
DR   GO; GO:0006886; P:intracellular protein transport; IEA:InterPro.
DR   GO; GO:0006890; P:retrograde vesicle-mediated transport, Golg. . .; TAS:UniProtKB.
DR   InterPro; IPR022775; AP_mu_sigma_su.
DR   InterPro; IPR000804; Clathrin_sm-chain_CS.
DR   InterPro; IPR011012; Longin-like.
DR   Pfam; PF01217; Clat_adaptor_s; 1.
DR   SUPFAM; SSF64356; Longin_like; 1.
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DR   PROSITE; PS00989; CLAT_ADAPTOR_S; 1.
PE   1: Evidence at protein level;
KW   Acetylation; Cytoplasm; Cytoplasmic vesicle;
KW   Direct protein sequencing; ER-Golgi transport; Golgi apparatus;
KW   Membrane; Phosphoprotein; Protein transport; Transport.
FT   CHAIN         1    177       Coatomer subunit zeta-1.
FT                                /FTId=PRO_0000193824.
FT   MOD_RES       1      1       N-acetylmethionine (By similarity).
FT   MOD_RES     161    161       Phosphoserine (By similarity).
FT   CONFLICT      7      7       E -> Q (in Ref. 1; CAA53539).
SQ   SEQUENCE   177 AA;  20228 MW;  D410249532C8BAF8 CRC64;

  Query Match             99.5%;  Score 878;  DB 1;  Length 177;
  Best Local Similarity   99.4%;
  Matches  176;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 MEALILEPSLYTVKAILILDNDGDRLFAKYYDDTYPSVKEQKAFEKNIFNKTHRTDSEIA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MEALILEPSLYTVKAILILDNDGDRLFAKYYDDTYPSVKEQKAFEKNIFNKTHRTDSEIA 60

Qy         61 LLEGLTVVYKSSIDLYFYVIGSSYENELMLMAVLNCLFDSLSQMLRKNVEKRALLENMEG 120
              |||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Db         61 LLEGLTVVYKSSIDLYFYVIGSSYENELMLMTVLNCLFDSLSQMLRKNVEKRALLENMEG 120

Qy        121 LFLAVDEIVDGGVILESDPQQVVHRVALRGEDVPLTEQTVSQVLQSAKEQIKWSLLR 177
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 LFLAVDEIVDGGVILESDPQQVVHRVALRGEDVPLTEQTVSQVLQSAKEQIKWSLLR 177


RESULT 7
Q53FU3_HUMAN
ID   Q53FU3_HUMAN            Unreviewed;       177 AA.
AC   Q53FU3;
DT   24-MAY-2005, integrated into UniProtKB/TrEMBL.
DT   24-MAY-2005, sequence version 1.
DT   05-OCT-2010, entry version 31.
DE   SubName: Full=Coatomer protein complex, subunit zeta 1 variant;
DE   Flags: Fragment;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
OC   Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Renal proximal tubule;
RX   MEDLINE=94171032; PubMed=8125298; DOI=10.1016/0378-1119(94)90802-8;
RA   Maruyama K., Sugano S.;
RT   "Oligo-capping: a simple method to replace the cap structure of
RT   eukaryotic mRNAs with oligoribonucleotides.";
RL   Gene 138:171-174(1994).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Renal proximal tubule;
RX   MEDLINE=98038986; PubMed=9373149; DOI=10.1016/S0378-1119(97)00411-3;
RA   Suzuki Y., Yoshitomo K., Maruyama K., Suyama A., Sugano S.;
RT   "Construction and characterization of a full length-enriched and a 5'-
RT   end-enriched cDNA library.";
RL   Gene 200:149-156(1997).
RN   [3]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Renal proximal tubule;
RA   Suzuki Y., Sugano S., Totoki Y., Toyoda A., Takeda T., Sakaki Y.,
RA   Tanaka A., Yokoyama S.;
RL   Submitted (APR-2005) to the EMBL/GenBank/DDBJ databases.
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CC   ----------------------------------------------------------------------
DR   EMBL; AK223188; BAD96908.1; -; mRNA.
DR   IPI; IPI00032851; -.
DR   UniGene; Hs.505652; -.
DR   STRING; Q53FU3; -.
DR   Ensembl; ENST00000262061; ENSP00000262061; ENSG00000111481.
DR   HGNC; HGNC:2243; COPZ1.
DR   HOVERGEN; HBG051077; -.
DR   ArrayExpress; Q53FU3; -.
DR   Bgee; Q53FU3; -.
DR   GO; GO:0030117; C:membrane coat; IEA:InterPro.
DR   GO; GO:0005515; F:protein binding; IEA:InterPro.
DR   GO; GO:0006886; P:intracellular protein transport; IEA:InterPro.
DR   GO; GO:0016192; P:vesicle-mediated transport; IEA:InterPro.
DR   InterPro; IPR022775; AP_mu_sigma_su.
DR   InterPro; IPR000804; Clathrin_sm-chain_CS.
DR   InterPro; IPR011012; Longin-like.
DR   Pfam; PF01217; Clat_adaptor_s; 1.
DR   SUPFAM; SSF64356; Longin_like; 1.
DR   PROSITE; PS00989; CLAT_ADAPTOR_S; 1.
PE   2: Evidence at transcript level;
FT   NON_TER       1      1
SQ   SEQUENCE   177 AA;  20267 MW;  5E2530D17696A10D CRC64;

  Query Match             99.4%;  Score 877;  DB 2;  Length 177;
  Best Local Similarity   99.4%;
  Matches  176;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 MEALILEPSLYTVKAILILDNDGDRLFAKYYDDTYPSVKEQKAFEKNIFNKTHRTDSEIA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MEALILEPSLYTVKAILILDNDGDRLFAKYYDDTYPSVKEQKAFEKNIFNKTHRTDSEIA 60

Qy         61 LLEGLTVVYKSSIDLYFYVIGSSYENELMLMAVLNCLFDSLSQMLRKNVEKRALLENMEG 120
              |||||||||||||||||||||||||||||||||||| ||||||||||||||||||
Db         61 LLEGLTVVYKSSIDLYFYVIGSSYENELMLMAVLNCLFDSLRQMLRKNVEKRALLENMEG 120

Qy        121 LFLAVDEIVDGGVILESDPQQVVHRVALRGEDVPLTEQTVSQVLQSAKEQIKWSLLR 177
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 LFLAVDEIVDGGVILESDPQQVVHRVALRGEDVPLTEQTVSQVLQSAKEQIKWSLLR 177


RESULT 8
Q28HL1_XENTR
ID   Q28HL1_XENTR            Unreviewed;       177 AA.
AC   Q28HL1;
DT   04-APR-2006, integrated into UniProtKB/TrEMBL.
DT   04-APR-2006, sequence version 1.
DT   05-OCT-2010, entry version 22.
DE   SubName: Full=OTTXETP00000008162;
GN   Name=copz1; ORFNames=TTpA002p21.1-001;
OS   Xenopus tropicalis (Western clawed frog) (Silurana tropicalis).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
OC   Xenopodinae; Xenopus; Silurana.
OX   NCBI_TaxID=8364;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Amaya E., Ashurst J.L., Bonfield J.K., Croning M.D.R., Chen C-K.,
RA   Davies R.M., Francis M.D., Garrett N., Gilchrist M.J., Grafham D.V.,
RA   McLaren S.R., Papalopulu N., Rogers J., Smith J.C., Taylor R.G.,
RA   Voigt J., Zorn A.M.;
RL   Submitted (OCT-2006) to the EMBL/GenBank/DDBJ databases.
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DR   EMBL; CR760836; CAJ83159.1; -; mRNA.
DR   UniGene; Str.5365; -.
DR   ProteinModelPortal; Q28HL1; -.
DR   SMR; Q28HL1; 1-149.
DR   STRING; Q28HL1; -.
DR   HOVERGEN; HBG051077; -.
DR   GO; GO:0030117; C:membrane coat; IEA:InterPro.
DR   GO; GO:0005515; F:protein binding; IEA:InterPro.
DR   GO; GO:0006886; P:intracellular protein transport; IEA:InterPro.
DR   GO; GO:0016192; P:vesicle-mediated transport; IEA:InterPro.
DR   InterPro; IPR022775; AP_mu_sigma_su.
DR   InterPro; IPR000804; Clathrin_sm-chain_CS.
DR   InterPro; IPR011012; Longin-like.
DR   Pfam; PF01217; Clat_adaptor_s; 1.
DR   SUPFAM; SSF64356; Longin_like; 1.
DR   PROSITE; PS00989; CLAT_ADAPTOR_S; 1.
PE   2: Evidence at transcript level;
SQ   SEQUENCE   177 AA;  20202 MW;  4739F11DFDBBD25E CRC64;

  Query Match             96.0%;  Score 847;  DB 2;  Length 177;
  Best Local Similarity   93.2%;
  Matches  165;  Conservative   11;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 MEALILEPSLYTVKAILILDNDGDRLFAKYYDDTYPSVKEQKAFEKNIFNKTHRTDSEIA 60
              |:|::|:||||||||:|||||||:||||||||:|||:|||||||||||||||||||||||
Db          1 MDAILLDPSLYTVKAVLILDNDGERLFAKYYDETYPTVKEQKAFEKNIFNKTHRTDSEIA 60

Qy         61 LLEGLTVVYKSSIDLYFYVIGSSYENELMLMAVLNCLFDSLSQMLRKNVEKRALLENMEG 120
              |||||||||||||||||||||:|||||||||||||||||||||||||||| |||||||
Db         61 LLEGLTVVYKSSIDLYFYVIGSSHENELMLMAVLNCLFDSLSQMLRKNVEKRTLLENMEG 120

Qy        121 LFLAVDEIVDGGVILESDPQQVVHRVALRGEDVPLTEQTVSQVLQSAKEQIKWSLLR 177
              ||||||||:|||||||||||||||||||:|||||||||||||||||||||||||||
Db        121 LFLAVDEIIDGGVILESDPQQVVHRVALRGDDVPLTEQTVSQVLQSAKEQIKWSLLR 177


RESULT 9
A0AUT9_XENLA
ID   A0AUT9_XENLA            Unreviewed;       177 AA.
AC   A0AUT9;
DT   28-NOV-2006, integrated into UniProtKB/TrEMBL.
DT   28-NOV-2006, sequence version 1.
DT   05-OCT-2010, entry version 17.
DE   SubName: Full=Copz1 protein;
GN   Name=Copz1;
OS   Xenopus laevis (African clawed frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
OC   Xenopodinae; Xenopus; Xenopus.
OX   NCBI_TaxID=8355;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC   TISSUE=Embryo;
RG   NIH - Xenopus Gene Collection (XGC) project;
RL   Submitted (OCT-2006) to the EMBL/GenBank/DDBJ databases.
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CC   ---------------------------------------------------------------------
DR   EMBL; BC124924; AAI24925.1; -; mRNA.
DR   UniGene; Xl.76078; -.
DR   ProteinModelPortal; A0AUT9; -.
DR   SMR; A0AUT9; 1-149.
DR   HOVERGEN; HBG051077; -.
DR   GO; GO:0030117; C:membrane coat; IEA:InterPro.
DR   GO; GO:0005515; F:protein binding; IEA:InterPro.
DR   GO; GO:0006886; P:intracellular protein transport; IEA:InterPro.
```

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DR   GO; GO:0016192; P:vesicle-mediated transport; IEA:InterPro.
DR   InterPro; IPR022775; AP_mu_sigma_su.
DR   InterPro; IPR000804; Clathrin_sm-chain_CS.
DR   InterPro; IPR011012; Longin-like.
DR   Pfam; PF01217; Clat_adaptor_s; 1.
DR   SUPFAM; SSF64356; Longin_like; 1.
DR   PROSITE; PS00989; CLAT_ADAPTOR_S; 1.
PE   2: Evidence at transcript level;
SQ   SEQUENCE   177 AA;  20188 MW;  529B50DAF6D85058 CRC64;

  Query Match             95.9%;  Score 846;  DB 2;  Length 177;
  Best Local Similarity   93.2%;
  Matches  165;  Conservative   11;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 MEALILEPSLYTVKAILILDNDGDRLFAKYYDDTYPSVKEQKAFEKNIFNKTHRTDSEIA 60
              |:|::|:||||||||:|||||||:||||||:|||:|||||||||||||||||||||||
Db          1 MDAVLLDPSLYTVKAVLILDNDGERLFAKYYDETYPTVKEQKAFEKNIFNKTHRTDSEIA 60

Qy         61 LLEGLTVVYKSSIDLYFYVIGSSYENELMLMAVLNCLFDSLSQMLRKNVEKRALLENMEG 120
              |||||||||||||||||||||:|||||||||||||||||||||||||||| |||||||
Db         61 LLEGLTVVYKSSIDLYFYVIGSSHENELMLMAVLNCLFDSLSQMLRKNVEKRTLLENMEG 120

Qy        121 LFLAVDEIVDGGVILESDPQQVVHRVALRGEDVPLTEQTVSQVLQSAKEQIKWSLLR 177
              ||||||||:||||||||||||||||:||||||||||||||||||||||||||||||
Db        121 LFLAVDEIIDGGVILESDPQQVVHRVALRGDDVPLTEQTVSQVLQSAKEQIKWSLLR 177


RESULT 10
Q801P3_XENLA
ID   Q801P3_XENLA            Unreviewed;       187 AA.
AC   Q801P3;
DT   01-JUN-2003, integrated into UniProtKB/TrEMBL.
DT   01-JUN-2003, sequence version 1.
DT   05-OCT-2010, entry version 29.
DE   SubName: Full=Copz1 protein;
DE   Flags: Fragment;
GN   Name=Copz1;
OS   Xenopus laevis (African clawed frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
OC   Xenopodinae; Xenopus; Xenopus.
OX   NCBI_TaxID=8355;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC   TISSUE=Embryo;
RG   NIH - Xenopus Gene Collection (XGC) project;
RL   Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; BC047988; AAH47988.1; -; mRNA.
DR   UniGene; Xl.76078; -.
DR   ProteinModelPortal; Q801P3; -.
DR   HOVERGEN; HBG051077; -.
DR   GO; GO:0030117; C:membrane coat; IEA:InterPro.
DR   GO; GO:0005515; F:protein binding; IEA:InterPro.
DR   GO; GO:0006886; P:intracellular protein transport; IEA:InterPro.
DR   GO; GO:0016192; P:vesicle-mediated transport; IEA:InterPro.
DR   InterPro; IPR022775; AP_mu_sigma_su.
DR   InterPro; IPR000804; Clathrin_sm-chain_CS.
DR   InterPro; IPR011012; Longin-like.
DR   Pfam; PF01217; Clat_adaptor_s; 1.
DR   SUPFAM; SSF64356; Longin_like; 1.
DR   PROSITE; PS00989; CLAT_ADAPTOR_S; 1.
PE   2: Evidence at transcript level;
FT   NON_TER       1      1
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SQ   SEQUENCE   187 AA;  21167 MW;  7BC34FFA40CA56E4 CRC64;

  Query Match             95.9%;  Score 846;  DB 2;  Length 187;
  Best Local Similarity   93.2%;
  Matches  165;  Conservative   11;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 MEALILEPSLYTVKAILILDNDGDRLFAKYYDDTYPSVKEQKAFEKNIFNKTHRTDSEIA 60
              |:|::|:||||||||:|||||||:||||||||:|||:|||||||||||||||||||||||
Db         11 MDAVLLDPSLYTVKAVLILDNDGERLFAKYYDETYPTVKEQKAFEKNIFNKTHRTDSEIA 70

Qy         61 LLEGLTVVYKSSIDLYFYVIGSSYENELMLMAVLNCLFDSLSQMLRKNVEKRALLENMEG 120
              |||||||||||||||||||:|||||||||||||||||||||||||||| |||||||
Db         71 LLEGLTVVYKSSIDLYFYVIGSSHENELMLMAVLNCLFDSLSQMLRKNVEKRTLLENMEG 130

Qy        121 LFLAVDEIVDGGVILESDPQQVVHRVALRGEDVPLTEQTVSQVLQSAKEQIKWSLLR 177
              ||||||||:|||||||||||||||||:||||||||||||||||||||||||||||||
Db        131 LFLAVDEIIDGGVILESDPQQVVHRVALRGDDVPLTEQTVSQVLQSAKEQIKWSLLR 187


RESULT 11
Q9IB48_DANRE
ID   Q9IB48_DANRE            Unreviewed;       177 AA.
AC   Q9IB48;
DT   01-OCT-2000, integrated into UniProtKB/TrEMBL.
DT   01-OCT-2000, sequence version 1.
DT   05-OCT-2010, entry version 48.
DE   SubName: Full=Nonclathrin coat protein zeta1-COP;
GN   Name=copz1;
OS   Danio rerio (Zebrafish) (Brachydanio rerio).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC   Cyprinidae; Danio.
OX   NCBI_TaxID=7955;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Hahn Y., Chung J.H.;
RT   "Identification of zeta-COP genes from various organisms.";
RL   Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; AB040044; BAA92783.1; -; mRNA.
DR   IPI; IPI00489034; -.
DR   RefSeq; NP_571583.1; -.
DR   UniGene; Dr.79072; -.
DR   ProteinModelPortal; Q9IB48; -.
DR   SMR; Q9IB48; 1-149.
DR   STRING; Q9IB48; -.
DR   Ensembl; ENSDART00000011201; ENSDARP00000015008; ENSDARG00000017844.
DR   GeneID; 57970; -.
DR   KEGG; dre:57970; -.
DR   NMPDR; fig|7955.3.peg.20733; -.
DR   CTD; 57970; -.
DR   ZFIN; ZDB-GENE-000406-6; copz1.
DR   HOVERGEN; HBG051077; -.
DR   InParanoid; Q9IB48; -.
DR   OMA; YDDTYPT; -.
DR   OrthoDB; EOG969TD6; -.
DR   PhylomeDB; Q9IB48; -.
DR   ArrayExpress; Q9IB48; -.
DR   Bgee; Q9IB48; -.
DR   GO; GO:0030117; C:membrane coat; IEA:InterPro.
DR   GO; GO:0005515; F:protein binding; IEA:InterPro.
DR   GO; GO:0006886; P:intracellular protein transport; IEA:InterPro.
DR   GO; GO:0002088; P:lens development in camera-type eye; IMP:ZFIN.
DR   GO; GO:0016192; P:vesicle-mediated transport; IEA:InterPro.
```

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DR   InterPro; IPR022775; AP_mu_sigma_su.
DR   InterPro; IPR000804; Clathrin_sm-chain_CS.
DR   InterPro; IPR011012; Longin-like.
DR   Pfam; PF01217; Clat_adaptor_s; 1.
DR   SUPFAM; SSF64356; Longin_like; 1.
DR   PROSITE; PS00989; CLAT_ADAPTOR_S; 1.
PE   2: Evidence at transcript level;
SQ   SEQUENCE   177 AA;  20279 MW;  EC44BED1889FEA07 CRC64;

  Query Match             95.8%;  Score 845;  DB 2;  Length 177;
  Best Local Similarity   93.2%;
  Matches  165;  Conservative   11;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 MEALILEPSLYTVKAILILDNDGDRLFAKYYDDTYPSVKEQKAFEKNIFNKTHRTDSEIA 60
              |: |||||||||||:||:||||:||:|||||||||:|||||||||||||||||||||||
Db          1 MDTLILEPSLYTVKAVLIMDNDGERLYAKYYDDTYPTVKEQKAFEKNIFNKTHRTDSEIA 60

Qy         61 LLEGLTVVYKSSIDLYFYVIGSSYENELMLMAVLNCLFDSLSQMLRKNVEKRALLENMEG 120
              ||||||||||:||||||||||:|||||||:|||||||||||||||||||||||||||||
Db         61 LLEGLTVVYKSNIDLYFYVIGSSHENELMLMSVLNCLFDSLSQMLRKNVEKRALLENMEG 120

Qy        121 LFLAVDEIVDGGVILESDPQQVVHRVALRGEDVPLTEQTVSQVLQSAKEQIKWSLLR 177
              |||||||||||||||||||||||||||||:|||||||||:|||||||||||||||||
Db        121 LFLAVDEIVDGGVILESDPQQVVHRVALRGDDVPLTEQTVTQVLQSAKEQIKWSLLR 177


RESULT 12
Q6GQG0_XENLA
ID   Q6GQG0_XENLA            Unreviewed;       177 AA.
AC   Q6GQG0;
DT   19-JUL-2004, integrated into UniProtKB/TrEMBL.
DT   19-JUL-2004, sequence version 1.
DT   05-OCT-2010, entry version 33.
DE   SubName: Full=MGC80093 protein;
GN   Name=copz1; Synonyms=MGC80093;
OS   Xenopus laevis (African clawed frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
OC   Xenopodinae; Xenopus; Xenopus.
OX   NCBI_TaxID=8355;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC   TISSUE=Spleen;
RG   NIH - Xenopus Gene Collection (XGC) project;
RL   Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
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CC   ---------------------------------------------------------------------
DR   EMBL; BC072784; AAH72784.1; -; mRNA.
DR   RefSeq; NP_001085450.1; -.
DR   UniGene; Xl.45820; -.
DR   ProteinModelPortal; Q6GQG0; -.
DR   SMR; Q6GQG0; 1-149.
DR   GeneID; 443876; -.
DR   KEGG; xla:443876; -.
DR   Xenbase; XB-GENE-6251726; copz1.
DR   HOVERGEN; HBG051077; -.
DR   GO; GO:0030117; C:membrane coat; IEA:InterPro.
DR   GO; GO:0005515; F:protein binding; IEA:InterPro.
DR   GO; GO:0006886; P:intracellular protein transport; IEA:InterPro.
DR   GO; GO:0016192; P:vesicle-mediated transport; IEA:InterPro.
DR   InterPro; IPR022775; AP_mu_sigma_su.
DR   InterPro; IPR000804; Clathrin_sm-chain_CS.
DR   InterPro; IPR011012; Longin-like.
DR   Pfam; PF01217; Clat_adaptor_s; 1.
DR   SUPFAM; SSF64356; Longin_like; 1.
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DR   PROSITE; PS00989; CLAT_ADAPTOR_S; 1.
PE   2: Evidence at transcript level;
SQ   SEQUENCE   177 AA;  20174 MW;  529B51DBF6D95158 CRC64;

  Query Match             95.6%;  Score 843;  DB 2;  Length 177;
  Best Local Similarity   92.7%;
  Matches  164;  Conservative   12;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 MEALILEPSLYTVKAILILDNDGDRLFAKYYDDTYPSVKEQKAFEKNIFNKTHRTDSEIA 60
              |:|::|:||||||||:|||||||:||||||:|||:||||||||||||||||||||||
Db          1 MDAVLLDPSLYTVKAVLILDNDGERLFAKYYDETYPTVKEQKAFEKNIFNKTHRTDSEIA 60

Qy         61 LLEGLTVVYKSSIDLYFYVIGSSYENELMLMAVLNCLFDSLSQMLRKNVEKRALLENMEG 120
              ||||||||||||||||||||:|||||||||||||||||||||||||||| |||||:|
Db         61 LLEGLTVVYKSSIDLYFYVIGSSHENELMLMAVLNCLFDSLSQMLRKNVEKRTLLENMDG 120

Qy        121 LFLAVDEIVDGGVILESDPQQVVHRVALRGEDVPLTEQTVSQVLQSAKEQIKWSLLR 177
              ||||||||:||||||||||||||||||:||||||||||||||||||||||||||||
Db        121 LFLAVDEIIDGGVILESDPQQVVHRVALRGDDVPLTEQTVSQVLQSAKEQIKWSLLR 177


RESULT 13
Q7SXH1_DANRE
ID   Q7SXH1_DANRE            Unreviewed;       177 AA.
AC   Q7SXH1;
DT   01-OCT-2003, integrated into UniProtKB/TrEMBL.
DT   01-OCT-2003, sequence version 1.
DT   05-OCT-2010, entry version 41.
DE   SubName: Full=Coatomer protein complex, subunit zeta 1;
GN   Name=copz1;
OS   Danio rerio (Zebrafish) (Brachydanio rerio).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC   Cyprinidae; Danio.
OX   NCBI_TaxID=7955;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC   TISSUE=Whole body;
RG   NIH - Zebrafish Gene Collection (ZGC) project;
RL   Submitted (AUG-2003) to the EMBL/GenBank/DDBJ databases.
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CC   ---------------------------------------------------------------------
DR   EMBL; BC055604; AAH55604.1; -; mRNA.
DR   IPI; IPI00489034; -.
DR   UniGene; Dr.79072; -.
DR   ProteinModelPortal; Q7SXH1; -.
DR   SMR; Q7SXH1; 1-149.
DR   STRING; Q7SXH1; -.
DR   PRIDE; Q7SXH1; -.
DR   Ensembl; ENSDART00000011201; ENSDARP00000015008; ENSDARG00000017844.
DR   ZFIN; ZDB-GENE-000406-6; copz1.
DR   eggNOG; fiNOG12172; -.
DR   HOGENOM; HBG326766; -.
DR   HOVERGEN; HBG051077; -.
DR   InParanoid; Q7SXH1; -.
DR   PhylomeDB; Q7SXH1; -.
DR   ArrayExpress; Q7SXH1; -.
DR   Bgee; Q7SXH1; -.
DR   GO; GO:0030117; C:membrane coat; IEA:InterPro.
DR   GO; GO:0005515; F:protein binding; IEA:InterPro.
DR   GO; GO:0006886; P:intracellular protein transport; IEA:InterPro.
DR   GO; GO:0016192; P:vesicle-mediated transport; IEA:InterPro.
DR   InterPro; IPR022775; AP_mu_sigma_su.
DR   InterPro; IPR000804; Clathrin_sm-chain_CS.
DR   InterPro; IPR011012; Longin-like.
```

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DR   Pfam; PF01217; Clat_adaptor_s; 1.
DR   SUPFAM; SSF64356; Longin_like; 1.
DR   PROSITE; PS00989; CLAT_ADAPTOR_S; 1.
PE   2: Evidence at transcript level;
SQ   SEQUENCE   177 AA;  20311 MW;  BC44BEC188939BDC CRC64;

  Query Match             95.5%;  Score 842;  DB 2;  Length 177;
  Best Local Similarity   92.7%;
  Matches  164;  Conservative   12;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 MEALILEPSLYTVKAILILDNDGDRLFAKYYDDTYPSVKEQKAFEKNIFNKTHRTDSEIA 60
              |: |||||||||||:||:||||:||:|||||||||:|||||||||||||||||||||||
Db          1 MDTLILEPSLYTVKAVLIMDNDGERLYAKYYDDTYPTVKEQKAFEKNIFNKTHRTDSEIA 60

Qy         61 LLEGLTVVYKSSIDLYFYVIGSSYENELMLMAVLNCLFDSLSQMLRKNVEKRALLENMEG 120
              |||||||:|||:||||||||||:|||||||:|||||||||||||||||||||||||||||
Db         61 LLEGLTVMYKSNIDLYFYVIGSSHENELMLMSVLNCLFDSLSQMLRKNVEKRALLENMEG 120

Qy        121 LFLAVDEIVDGGVILESDPQQVVHRVALRGEDVPLTEQTVSQVLQSAKEQIKWSLLR 177
              |||||||||||||||||||||||||||||:|||||||||:|||||||||||||||||
Db        121 LFLAVDEIVDGGVILESDPQQVVHRVALRGDDVPLTEQTVTQVLQSAKEQIKWSLLR 177


RESULT 14
C3KJY4_ANOFI
ID   C3KJY4_ANOFI            Unreviewed;       177 AA.
AC   C3KJY4;
DT   16-JUN-2009, integrated into UniProtKB/TrEMBL.
DT   16-JUN-2009, sequence version 1.
DT   05-OCT-2010, entry version 8.
DE   SubName: Full=Coatomer subunit zeta-1;
GN   Name=COPZ1;
OS   Anoplopoma fimbria (Sablefish).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC   Acanthomorpha; Acanthopterygii; Percomorpha; Scorpaeniformes;
OC   Anoplopomatoidei; Anoplopomatidae; Anoplopoma.
OX   NCBI_TaxID=229290;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Brain;
RA   Messmer A., Rondeau E., Sanderson D., Cooper G., Leong J., Koop B.F.;
RT   "Anoplopoma fimbria ESTs and full-length cDNAs.";
RL   Submitted (MAY-2009) to the EMBL/GenBank/DDBJ databases.
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CC   ---------------------------------------------------------------------
DR   EMBL; BT083249; ACQ58956.1; -; mRNA.
DR   GO; GO:0006810; P:transport; IEA:InterPro.
DR   InterPro; IPR022775; AP_mu_sigma_su.
DR   InterPro; IPR011012; Longin-like.
DR   Pfam; PF01217; Clat_adaptor_s; 1.
DR   SUPFAM; SSF64356; Longin_like; 1.
PE   2: Evidence at transcript level;
SQ   SEQUENCE   177 AA;  20187 MW;  E665075A8B25F591 CRC64;

  Query Match             94.8%;  Score 836;  DB 2;  Length 177;
  Best Local Similarity   92.7%;
  Matches  164;  Conservative   12;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 MEALILEPSLYTVKAILILDNDGDRLFAKYYDDTYPSVKEQKAFEKNIFNKTHRTDSEIA 60
              |:: ||||||:||||:||||||||||:|||||||||:|||||||||||||||||||||||
Db          1 MDSPILEPSLHTVKAVLILDNDGDRLYAKYYDDTYPTVKEQKAFEKNIFNKTHRTDSEIA 60

Qy         61 LLEGLTVVYKSSIDLYFYVIGSSYENELMLMAVLNCLFDSLSQMLRKNVEKRALLENMEG 120
              ||||||||||:|||:|||||||:|||||||||||||||||||||||||||||||||||||
```

```
Db         61 LLEGLTVVYKSNIDLFFYVIGSSHENELMLMAVLNCLFDSLSQMLRKNVERRALLENMEG 120

Qy        121 LFLAVDEIVDGGVILESDPQQVVHRVALRGEDVPLTEQTVSQVLQSAKEQIKWSLLR 177
              ||||||||||||||||||||||||||||:|||||||||:||||||||||||||||
Db        121 LFLAVDEIVDGGVILESDPQQVVHRVALRGDDVPLTEQTVTQVLQSAKEQIKWSLLR 177


RESULT 15
B5X5K5_SALSA
ID   B5X5K5_SALSA            Unreviewed;       177 AA.
AC   B5X5K5;
DT   25-NOV-2008, integrated into UniProtKB/TrEMBL.
DT   25-NOV-2008, sequence version 1.
DT   02-NOV-2010, entry version 10.
DE   SubName: Full=Coatomer subunit zeta-1;
GN   Name=COPZ1;
OS   Salmo salar (Atlantic salmon).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC   Protacanthopterygii; Salmoniformes; Salmonidae; Salmoninae; Salmo.
OX   NCBI_TaxID=8030;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Brain;
RX   PubMed=20433749; DOI=10.1186/1471-2164-11-279;
RA   Leong J.S., Jantzen S.G., von Schalburg K.R., Cooper G.A.,
RA   Messmer A.M., Liao N.Y., Munro S., Moore R., Holt R.A., Jones S.J.,
RA   Davidson W.S., Koop B.F.;
RT   "Salmo salar and Esox lucius full-length cDNA sequences reveal changes
RT   in evolutionary pressures on a post-tetraploidization genome.";
RL   BMC Genomics 11:279-279(2010).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Brain;
RG   cGRASP (B.F. Koop & W.S. Davidson);
RA   Leong J., von Schalburg K., Cooper G., Moore R., Holt R.,
RA   Davidson W.S., Koop B.F.;
RL   Submitted (OCT-2008) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Brain;
RG   cGRASP (B.F. Koop & W.S. Davidson);
RL   Submitted (AUG-2010) to the EMBL/GenBank/DDBJ databases.
RN   [4]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Mixed brain;
RG   cGRASP (B.F. Koop & W.S. Davidson);
RA   Leong J., von Schalburg K., Cooper G., Moore R., Holt R.,
RA   Davidson W.S., Koop B.F.;
RT   "Salmo salar full-length cDNAs.";
RL   Submitted (FEB-2009) to the EMBL/GenBank/DDBJ databases.
RN   [5]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Brain;
RG   cGRASP (B.F. Koop & W.S. Davidson);
RA   Leong J., von Schalburg K., Cooper G., Moore R., Holt R.,
RA   Davidson W.S., Koop B.F.;
RL   Submitted (FEB-2009) to the EMBL/GenBank/DDBJ databases.
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CC   ---------------------------------------------------------------------
DR   EMBL; BT046324; ACI66125.1; -; mRNA.
DR   EMBL; BT058392; ACN10105.1; -; mRNA.
DR   EMBL; BT060094; ACN12454.1; -; mRNA.
DR   HOVERGEN; HBG051077; -.
DR   GO; GO:0030117; C:membrane coat; IEA:InterPro.
```

```
DR   GO; GO:0005515; F:protein binding; IEA:InterPro.
DR   GO; GO:0006886; P:intracellular protein transport; IEA:InterPro.
DR   GO; GO:0016192; P:vesicle-mediated transport; IEA:InterPro.
DR   InterPro; IPR022775; AP_mu_sigma_su.
DR   InterPro; IPR000804; Clathrin_sm-chain_CS.
DR   InterPro; IPR011012; Longin-like.
DR   Pfam; PF01217; Clat_adaptor_s; 1.
DR   SUPFAM; SSF64356; Longin_like; 1.
DR   PROSITE; PS00989; CLAT_ADAPTOR_S; 1.
PE   2: Evidence at transcript level;
SQ   SEQUENCE   177 AA;  20273 MW;  2BBAC0388F6E8E69 CRC64;

  Query Match             94.3%;  Score 832;  DB 2;  Length 177;
  Best Local Similarity   92.1%;
  Matches  163;  Conservative   13;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 MEALILEPSLYTVKAILILDNDGDRLFAKYYDDTYPSVKEQKAFEKNIFNKTHRTDSEIA 60
              |:|| |||:|||||:|||||||:||:|||||:|||:|||||||||||||||||||||||
Db          1 MDALSLEPTLYTVKAVLILDNDGERLYAKYYDETYPTVKEQKAFEKNIFNKTHRTDSEIA 60

Qy         61 LLEGLTVVYKSSIDLYFYVIGSSYENELMLMAVLNCLFDSLSQMLRKNVEKRALLENMEG 120
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Db         61 LLEGLTVVYKSNIDLYFYVIGSSHENELMLMSVLNCLFDSLSQMLRKNVERRALLENMEG 120

Qy        121 LFLAVDEIVDGGVILESDPQQVVHRVALRGEDVPLTEQTVSQVLQSAKEQIKWSLLR 177
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Db        121 LFLAVDEIVDGGVILESDPQQVVYRVALRGDDVPLTEQTVSQVLQSAKEQIKWSLLR 177


Search completed: December 14, 2010, 11:27:05
Job time : 96.872 secs
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SCORE 3.0

SCORE Search Results Details for Application 09556178 and Search Result 20101214_103256_us-09-556-178-5.rapbm.

Score Home Page Retrieve Application List SCORE System Overview SCORE FAQ Comments / Suggestions

This page gives you Search Results detail for the Application 09556178 and Search Result 20101214_103256_us-09-556-178-5.rapbm.

Go Back to previous page

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                        GenCore version 6.3
                  Copyright (c) 1993 - 2010  Biocceleration Ltd.


OM protein - protein search, using sw model

Run on:          December 14, 2010, 11:27:17 ; Search time 143 Seconds
                                             (without alignments)
                                             1680.685 Million cell updates/sec

Title:           US-09-556-178-5
Perfect score:   882
Sequence:        1 MEALILEPSLYTVKAILILD.........QTVSQVLQSAKEQIKWSLLR 177

Scoring table:   BLOSUM62
                 Gapop 10.0 , Gapext 0.5

Searched:        6210261 seqs, 1354514112 residues

Total number of hits satisfying chosen parameters:      6210261

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :        Published_Applications_AA_Main:*
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                 2:  /ABSS/Data/CRF/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
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                 4:  /ABSS/Data/CRF/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
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Result           Query
   No.    Score  Match Length DB  ID                          Description
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     1      882  100.0    177  5  US-10-528-183-26            Sequence 26, Appl
     2      882  100.0    177  6  US-11-371-354-73107         Sequence 73107, A
     3      882  100.0    177  6  US-11-443-428A-819809       Sequence 819809,
     4      882  100.0    177  7  US-11-597-825-1351          Sequence 1351, Ap
     5      882  100.0    177  8  US-12-399-906-29            Sequence 29, Appl
     6      882  100.0    192  6  US-11-443-428A-819804       Sequence 819804,
     7      882  100.0    192  6  US-11-443-428A-819805       Sequence 819805,
     8      882  100.0    192  6  US-11-443-428A-819806       Sequence 819806,
     9      882  100.0    192  6  US-11-443-428A-819808       Sequence 819808,
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10	882	100.0	192	6	US-11-443-428A-819810	Sequence 819810,
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13	882	100.0	192	6	US-11-443-428A-819819	Sequence 819819,
14	882	100.0	192	6	US-11-443-428A-819821	Sequence 819821,
15	882	100.0	192	6	US-11-443-428A-819823	Sequence 819823,
16	882	100.0	192	6	US-11-443-428A-819825	Sequence 819825,
17	882	100.0	200	6	US-11-443-428A-819807	Sequence 819807,
18	882	100.0	205	6	US-11-443-428A-819812	Sequence 819812,
19	868	98.4	182	6	US-11-443-428A-819814	Sequence 819814,
20	858	97.3	172	6	US-11-443-428A-819813	Sequence 819813,
21	856	97.1	177	6	US-11-443-428A-819815	Sequence 819815,
22	856	97.1	178	6	US-11-443-428A-819811	Sequence 819811,
23	845	95.8	177	4	US-10-403-571-30	Sequence 30, Appl
24	712	80.7	144	4	US-10-425-115-275189	Sequence 275189,
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26	701	79.5	173	6	US-11-443-428A-819820	Sequence 819820,
27	673	76.3	210	5	US-10-528-183-14	Sequence 14, Appl
28	673	76.3	210	5	US-10-743-643-2465	Sequence 2465, Ap
29	673	76.3	210	6	US-11-371-354-59225	Sequence 59225, A
30	673	76.3	210	8	US-12-399-906-30	Sequence 30, Appl
31	673	76.3	214	6	US-11-443-428A-823399	Sequence 823399,
32	564.5	64.0	160	6	US-11-097-143-7677	Sequence 7677, Ap
33	542	61.5	134	6	US-11-443-428A-819826	Sequence 819826,
34	518	58.7	136	6	US-11-443-428A-823401	Sequence 823401,
35	510	57.8	169	6	US-11-443-428A-823406	Sequence 823406,
36	507.5	57.5	181	7	US-11-360-355-120385	Sequence 120385,
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38	507.5	57.5	181	8	US-12-101-830-120385	Sequence 120385,
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42	441.5	50.1	154	7	US-11-360-355-123790	Sequence 123790,
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44	440	49.9	99	3	US-09-925-297-776	Sequence 776, App
45	440	49.9	125	6	US-11-443-428A-819817	Sequence 819817,

ALIGNMENTS

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RESULT 1
US-10-528-183-26
; Sequence 26, Application US/10528183
; Publication No. US20050226879A1
; GENERAL INFORMATION:
;  APPLICANT: Ullman, Katharine
;  APPLICANT:  Liu, Jin
;  APPLICANT:  Prunuske, Amy
;  APPLICANT:  Dimaano, Christian
;  TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATED TO
;  TITLE OF INVENTION:  INHIBITING NUCLEAR ENVELOPE BREAKDOWN
;  FILE REFERENCE: 21101.0045U2
;  CURRENT APPLICATION NUMBER: US/10/528,183
;  CURRENT FILING DATE:  2005-03-17
;  PRIOR APPLICATION NUMBER: PCT/US03/29267
;  PRIOR FILING DATE: 2003-09-17
;  PRIOR APPLICATION NUMBER: 60/411,248
;  PRIOR FILING DATE: 2002-09-17
;  NUMBER OF SEQ ID NOS: 35
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 26
;   LENGTH: 177
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:/note =
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;   OTHER INFORMATION: synthetic construct
US-10-528-183-26

  Query Match             100.0%;  Score 882;  DB 5;  Length 177;
  Best Local Similarity   100.0%;
  Matches  177;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Db         61 LLEGLTVVYKSSIDLYFYVIGSSYENELMLMAVLNCLFDSLSQMLRKNVEKRALLENMEG 120

Qy        121 LFLAVDEIVDGGVILESDPQQVVHRVALRGEDVPLTEQTVSQVLQSAKEQIKWSLLR 177
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 LFLAVDEIVDGGVILESDPQQVVHRVALRGEDVPLTEQTVSQVLQSAKEQIKWSLLR 177


RESULT 2
US-11-371-354-73107
; Sequence 73107, Application US/11371354
; Publication No. US20060275794A1
; GENERAL INFORMATION:
;  APPLICANT: CARRINO, JOHN
;  APPLICANT:  LIANG, FENG
;  TITLE OF INVENTION: COLLECTIONS OF MATCHED BIOLOGICAL REAGENTS AND METHODS FOR
;  TITLE OF INVENTION:  IDENTIFYING MATCHED REAGENTS
;  FILE REFERENCE: INV-1005-UT2
;  CURRENT APPLICATION NUMBER: US/11/371,354
;  CURRENT FILING DATE:  2006-03-07
;  PRIOR APPLICATION NUMBER: 60/673,045
;  PRIOR FILING DATE: 2005-04-19
;  PRIOR APPLICATION NUMBER: 60/665,199
;  PRIOR FILING DATE: 2005-03-25
;  PRIOR APPLICATION NUMBER: 60/665,200
;  PRIOR FILING DATE: 2005-03-25
;  PRIOR APPLICATION NUMBER: 60/659,493
;  PRIOR FILING DATE: 2005-03-07
;  PRIOR APPLICATION NUMBER: 60/659,492
;  PRIOR FILING DATE: 2005-03-07
;  PRIOR APPLICATION NUMBER: 60/953,586
;  PRIOR FILING DATE: 2005-02-15
;  PRIOR APPLICATION NUMBER: 60/651,390
;  PRIOR FILING DATE: 2005-02-08
;  NUMBER OF SEQ ID NOS: 78682
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 73107
;   LENGTH: 177
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-11-371-354-73107

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RESULT 3
US-11-443-428A-819809
; Sequence 819809, Application US/11443428A
; Publication No. US20070083334A1
; GENERAL INFORMATION:
;  APPLICANT: Mintz, Liat
;  APPLICANT:  Xie, Hanqing
;  APPLICANT:  Dahari, Dvir
;  APPLICANT:  Levanon, Erez
;  APPLICANT:  Freilich, Shiri
;  APPLICANT:  Beck, Nili
;  APPLICANT:  Zhu, Wei-Yong
;  APPLICANT:  Wasserman, Alon
;  APPLICANT:  Hermesh, Chen
;  APPLICANT:  Azar, Idit
;  APPLICANT:  Bernstein, Jeanne
;  TITLE OF INVENTION: METHODS AND SYSTEMS USEFUL FOR ANNOTATING BIOMOLECULAR SEQUENCES
;  FILE REFERENCE: 02/23929
;  CURRENT APPLICATION NUMBER: US/11/443,428A
;  CURRENT FILING DATE:  2006-05-31
;  NUMBER OF SEQ ID NOS: 1034312
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 819809
;   LENGTH: 177
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-11-443-428A-819809

  Query Match             100.0%;  Score 882;  DB 6;  Length 177;
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Qy          1 MEALILEPSLYTVKAILILDNDGDRLFAKYYDDTYPSVKEQKAFEKNIFNKTHRTDSEIA 60
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Qy         61 LLEGLTVVYKSSIDLYFYVIGSSYENELMLMAVLNCLFDSLSQMLRKNVEKRALLENMEG 120
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Db         61 LLEGLTVVYKSSIDLYFYVIGSSYENELMLMAVLNCLFDSLSQMLRKNVEKRALLENMEG 120

Qy        121 LFLAVDEIVDGGVILESDPQQVVHRVALRGEDVPLTEQTVSQVLQSAKEQIKWSLLR 177
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Db        121 LFLAVDEIVDGGVILESDPQQVVHRVALRGEDVPLTEQTVSQVLQSAKEQIKWSLLR 177


RESULT 4
US-11-597-825-1351
; Sequence 1351, Application US/11597825
; Publication No. US20090297536A1
; GENERAL INFORMATION:
;  APPLICANT: CHIN, Lynda
;  TITLE OF INVENTION: COMPOSITIONS, KITS, AND METHODS FOR
;  TITLE OF INVENTION:  IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY OF
;  TITLE OF INVENTION:  CANCER
;  FILE REFERENCE: DFN-059-2
;  CURRENT APPLICATION NUMBER: US/11/597,825
;  CURRENT FILING DATE:  2006-11-27
;  NUMBER OF SEQ ID NOS: 1528
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1351
;   LENGTH: 177
;   TYPE: PRT
;   ORGANISM: Homo sapiens
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US-11-597-825-1351

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Qy         61 LLEGLTVVYKSSIDLYFYVIGSSYENELMLMAVLNCLFDSLSQMLRKNVEKRALLENMEG 120
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Qy        121 LFLAVDEIVDGGVILESDPQQVVHRVALRGEDVPLTEQTVSQVLQSAKEQIKWSLLR 177
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RESULT 5
US-12-399-906-29
; Sequence 29, Application US/12399906
; Publication No. US20100226856A1
; GENERAL INFORMATION
;  APPLICANT: Vitaliano, Franco
;  APPLICANT:Vitaliano, Gordana D
;  TITLE OF INVENTION: DYNAMIC BIO-NANOPARTICLE ELEMENTS
;  FILE REFERENCE: FV3011
;  CURRENT APPLICATION NUMBER: US/12/399,906
;  CURRENT FILING DATE: 2009-09-23
;  NUMBER OF SEQ ID NOS: 30
;  SOFTWARE: PatentIn version 3.5
; SEQ ID NO 29
;  LENGTH: 177
;  TYPE: PRT
;  ORGANISM: Homo sapiens
;  PUBLICATION INFORMATION:
;  DATABASE ACCESSION NUMBER: UniProtKB/P61923
;  DATABASE ENTRY DATE: 2009-05-05
;  RELEVANT RESIDUES IN SEQ ID NO: (1)..(177)
US-12-399-906-29

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Qy          1 MEALILEPSLYTVKAILILDNDGDRLFAKYYDDTYPSVKEQKAFEKNIFNKTHRTDSEIA 60
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Db          1 MEALILEPSLYTVKAILILDNDGDRLFAKYYDDTYPSVKEQKAFEKNIFNKTHRTDSEIA 60

Qy         61 LLEGLTVVYKSSIDLYFYVIGSSYENELMLMAVLNCLFDSLSQMLRKNVEKRALLENMEG 120
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Db         61 LLEGLTVVYKSSIDLYFYVIGSSYENELMLMAVLNCLFDSLSQMLRKNVEKRALLENMEG 120

Qy        121 LFLAVDEIVDGGVILESDPQQVVHRVALRGEDVPLTEQTVSQVLQSAKEQIKWSLLR 177
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RESULT 6
US-11-443-428A-819804
; Sequence 819804, Application US/11443428A
; Publication No. US20070083334A1
; GENERAL INFORMATION:
;  APPLICANT: Mintz, Liat
;  APPLICANT:  Xie, Hanqing
;  APPLICANT:  Dahari, Dvir
```

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;  APPLICANT:  Levanon, Erez
;  APPLICANT:  Freilich, Shiri
;  APPLICANT:  Beck, Nili
;  APPLICANT:  Zhu, Wei-Yong
;  APPLICANT:  Wasserman, Alon
;  APPLICANT:  Hermesh, Chen
;  APPLICANT:  Azar, Idit
;  APPLICANT:  Bernstein, Jeanne
;  TITLE OF INVENTION: METHODS AND SYSTEMS USEFUL FOR ANNOTATING BIOMOLECULAR SEQUENCES
;  FILE REFERENCE: 02/23929
;  CURRENT APPLICATION NUMBER: US/11/443,428A
;  CURRENT FILING DATE:  2006-05-31
;  NUMBER OF SEQ ID NOS: 1034312
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 819804
;   LENGTH: 192
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-11-443-428A-819804

  Query Match             100.0%;  Score 882;  DB 6;  Length 192;
  Best Local Similarity   100.0%;
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Qy          1 MEALILEPSLYTVKAILILDNDGDRLFAKYYDDTYPSVKEQKAFEKNIFNKTHRTDSEIA 60
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Qy         61 LLEGLTVVYKSSIDLYFYVIGSSYENELMLMAVLNCLFDSLSQMLRKNVEKRALLENMEG 120
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Db         76 LLEGLTVVYKSSIDLYFYVIGSSYENELMLMAVLNCLFDSLSQMLRKNVEKRALLENMEG 135

Qy        121 LFLAVDEIVDGGVILESDPQQVVHRVALRGEDVPLTEQTVSQVLQSAKEQIKWSLLR 177
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        136 LFLAVDEIVDGGVILESDPQQVVHRVALRGEDVPLTEQTVSQVLQSAKEQIKWSLLR 192


RESULT 7
US-11-443-428A-819805
; Sequence 819805, Application US/11443428A
; Publication No. US20070083334A1
; GENERAL INFORMATION:
;  APPLICANT: Mintz, Liat
;  APPLICANT:  Xie, Hanqing
;  APPLICANT:  Dahari, Dvir
;  APPLICANT:  Levanon, Erez
;  APPLICANT:  Freilich, Shiri
;  APPLICANT:  Beck, Nili
;  APPLICANT:  Zhu, Wei-Yong
;  APPLICANT:  Wasserman, Alon
;  APPLICANT:  Hermesh, Chen
;  APPLICANT:  Azar, Idit
;  APPLICANT:  Bernstein, Jeanne
;  TITLE OF INVENTION: METHODS AND SYSTEMS USEFUL FOR ANNOTATING BIOMOLECULAR SEQUENCES
;  FILE REFERENCE: 02/23929
;  CURRENT APPLICATION NUMBER: US/11/443,428A
;  CURRENT FILING DATE:  2006-05-31
;  NUMBER OF SEQ ID NOS: 1034312
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 819805
;   LENGTH: 192
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-11-443-428A-819805

  Query Match             100.0%;  Score 882;  DB 6;  Length 192;
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Db         76 LLEGLTVVYKSSIDLYFYVIGSSYENELMLMAVLNCLFDSLSQMLRKNVEKRALLENMEG 135

Qy        121 LFLAVDEIVDGGVILESDPQQVVHRVALRGEDVPLTEQTVSQVLQSAKEQIKWSLLR 177
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; Sequence 819806, Application US/11443428A
; Publication No. US20070083334A1
; GENERAL INFORMATION:
;  APPLICANT: Mintz, Liat
;  APPLICANT:  Xie, Hanqing
;  APPLICANT:  Dahari, Dvir
;  APPLICANT:  Levanon, Erez
;  APPLICANT:  Freilich, Shiri
;  APPLICANT:  Beck, Nili
;  APPLICANT:  Zhu, Wei-Yong
;  APPLICANT:  Wasserman, Alon
;  APPLICANT:  Hermesh, Chen
;  APPLICANT:  Azar, Idit
;  APPLICANT:  Bernstein, Jeanne
;  TITLE OF INVENTION: METHODS AND SYSTEMS USEFUL FOR ANNOTATING BIOMOLECULAR SEQUENCES
;  FILE REFERENCE: 02/23929
;  CURRENT APPLICATION NUMBER: US/11/443,428A
;  CURRENT FILING DATE:  2006-05-31
;  NUMBER OF SEQ ID NOS: 1034312
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 819806
;   LENGTH: 192
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-11-443-428A-819806

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  Matches  177;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Db        136 LFLAVDEIVDGGVILESDPQQVVHRVALRGEDVPLTEQTVSQVLQSAKEQIKWSLLR 192


RESULT 9
US-11-443-428A-819808
; Sequence 819808, Application US/11443428A
; Publication No. US20070083334A1
; GENERAL INFORMATION:
;  APPLICANT: Mintz, Liat
;  APPLICANT:  Xie, Hanqing
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;  APPLICANT:  Dahari, Dvir
;  APPLICANT:  Levanon, Erez
;  APPLICANT:  Freilich, Shiri
;  APPLICANT:  Beck, Nili
;  APPLICANT:  Zhu, Wei-Yong
;  APPLICANT:  Wasserman, Alon
;  APPLICANT:  Hermesh, Chen
;  APPLICANT:  Azar, Idit
;  APPLICANT:  Bernstein, Jeanne
;  TITLE OF INVENTION: METHODS AND SYSTEMS USEFUL FOR ANNOTATING BIOMOLECULAR SEQUENCES
;  FILE REFERENCE: 02/23929
;  CURRENT APPLICATION NUMBER: US/11/443,428A
;  CURRENT FILING DATE:  2006-05-31
;  NUMBER OF SEQ ID NOS: 1034312
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 819808
;   LENGTH: 192
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-11-443-428A-819808

  Query Match             100.0%;  Score 882;  DB 6;  Length 192;
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  Matches  177;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MEALILEPSLYTVKAILILDNDGDRLFAKYYDDTYPSVKEQKAFEKNIFNKTHRTDSEIA 60
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Db        136 LFLAVDEIVDGGVILESDPQQVVHRVALRGEDVPLTEQTVSQVLQSAKEQIKWSLLR 192


RESULT 10
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; Sequence 819810, Application US/11443428A
; Publication No. US20070083334A1
; GENERAL INFORMATION:
;  APPLICANT: Mintz, Liat
;  APPLICANT:  Xie, Hanqing
;  APPLICANT:  Dahari, Dvir
;  APPLICANT:  Levanon, Erez
;  APPLICANT:  Freilich, Shiri
;  APPLICANT:  Beck, Nili
;  APPLICANT:  Zhu, Wei-Yong
;  APPLICANT:  Wasserman, Alon
;  APPLICANT:  Hermesh, Chen
;  APPLICANT:  Azar, Idit
;  APPLICANT:  Bernstein, Jeanne
;  TITLE OF INVENTION: METHODS AND SYSTEMS USEFUL FOR ANNOTATING BIOMOLECULAR SEQUENCES
;  FILE REFERENCE: 02/23929
;  CURRENT APPLICATION NUMBER: US/11/443,428A
;  CURRENT FILING DATE:  2006-05-31
;  NUMBER OF SEQ ID NOS: 1034312
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 819810
;   LENGTH: 192
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-11-443-428A-819810

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RESULT 11
US-11-443-428A-819816
; Sequence 819816, Application US/11443428A
; Publication No. US20070083334A1
; GENERAL INFORMATION:
;  APPLICANT: Mintz, Liat
;  APPLICANT:  Xie, Hanqing
;  APPLICANT:  Dahari, Dvir
;  APPLICANT:  Levanon, Erez
;  APPLICANT:  Freilich, Shiri
;  APPLICANT:  Beck, Nili
;  APPLICANT:  Zhu, Wei-Yong
;  APPLICANT:  Wasserman, Alon
;  APPLICANT:  Hermesh, Chen
;  APPLICANT:  Azar, Idit
;  APPLICANT:  Bernstein, Jeanne
;  TITLE OF INVENTION: METHODS AND SYSTEMS USEFUL FOR ANNOTATING BIOMOLECULAR SEQUENCES
;  FILE REFERENCE: 02/23929
;  CURRENT APPLICATION NUMBER: US/11/443,428A
;  CURRENT FILING DATE:  2006-05-31
;  NUMBER OF SEQ ID NOS: 1034312
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 819816
;   LENGTH: 192
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-11-443-428A-819816

  Query Match             100.0%;  Score 882;  DB 6;  Length 192;
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  Matches  177;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MEALILEPSLYTVKAILILDNDGDRLFAKYYDDTYPSVKEQKAFEKNIFNKTHRTDSEIA 60
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RESULT 12
US-11-443-428A-819818
; Sequence 819818, Application US/11443428A
; Publication No. US20070083334A1
; GENERAL INFORMATION:
;  APPLICANT: Mintz, Liat
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;  APPLICANT:  Xie, Hanqing
;  APPLICANT:  Dahari, Dvir
;  APPLICANT:  Levanon, Erez
;  APPLICANT:  Freilich, Shiri
;  APPLICANT:  Beck, Nili
;  APPLICANT:  Zhu, Wei-Yong
;  APPLICANT:  Wasserman, Alon
;  APPLICANT:  Hermesh, Chen
;  APPLICANT:  Azar, Idit
;  APPLICANT:  Bernstein, Jeanne
;  TITLE OF INVENTION: METHODS AND SYSTEMS USEFUL FOR ANNOTATING BIOMOLECULAR SEQUENCES
;  FILE REFERENCE: 02/23929
;  CURRENT APPLICATION NUMBER: US/11/443,428A
;  CURRENT FILING DATE:  2006-05-31
;  NUMBER OF SEQ ID NOS: 1034312
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 819818
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;   ORGANISM: Homo sapiens
US-11-443-428A-819818

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Qy         61 LLEGLTVVYKSSIDLYFYVIGSSYENELMLMAVLNCLFDSLSQMLRKNVEKRALLENMEG 120
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Qy        121 LFLAVDEIVDGGVILESDPQQVVHRVALRGEDVPLTEQTVSQVLQSAKEQIKWSLLR 177
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RESULT 13
US-11-443-428A-819819
; Sequence 819819, Application US/11443428A
; Publication No. US20070083334A1
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;  APPLICANT: Mintz, Liat
;  APPLICANT:  Xie, Hanqing
;  APPLICANT:  Dahari, Dvir
;  APPLICANT:  Levanon, Erez
;  APPLICANT:  Freilich, Shiri
;  APPLICANT:  Beck, Nili
;  APPLICANT:  Zhu, Wei-Yong
;  APPLICANT:  Wasserman, Alon
;  APPLICANT:  Hermesh, Chen
;  APPLICANT:  Azar, Idit
;  APPLICANT:  Bernstein, Jeanne
;  TITLE OF INVENTION: METHODS AND SYSTEMS USEFUL FOR ANNOTATING BIOMOLECULAR SEQUENCES
;  FILE REFERENCE: 02/23929
;  CURRENT APPLICATION NUMBER: US/11/443,428A
;  CURRENT FILING DATE:  2006-05-31
;  NUMBER OF SEQ ID NOS: 1034312
;  SOFTWARE: PatentIn version 3.1
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;   LENGTH: 192
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-11-443-428A-819819
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Qy          1 MEALILEPSLYTVKAILILDNDGDRLFAKYYDDTYPSVKEQKAFEKNIFNKTHRTDSEIA 60
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; Sequence 819821, Application US/11443428A
; Publication No. US20070083334A1
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;  APPLICANT:  Xie, Hanqing
;  APPLICANT:  Dahari, Dvir
;  APPLICANT:  Levanon, Erez
;  APPLICANT:  Freilich, Shiri
;  APPLICANT:  Beck, Nili
;  APPLICANT:  Zhu, Wei-Yong
;  APPLICANT:  Wasserman, Alon
;  APPLICANT:  Hermesh, Chen
;  APPLICANT:  Azar, Idit
;  APPLICANT:  Bernstein, Jeanne
;  TITLE OF INVENTION: METHODS AND SYSTEMS USEFUL FOR ANNOTATING BIOMOLECULAR SEQUENCES
;  FILE REFERENCE: 02/23929
;  CURRENT APPLICATION NUMBER: US/11/443,428A
;  CURRENT FILING DATE:  2006-05-31
;  NUMBER OF SEQ ID NOS: 1034312
;  SOFTWARE: PatentIn version 3.1
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;   ORGANISM: Homo sapiens
US-11-443-428A-819821

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Db         16 MEALILEPSLYTVKAILILDNDGDRLFAKYYDDTYPSVKEQKAFEKNIFNKTHRTDSEIA 75

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; Publication No. US20070083334A1
; GENERAL INFORMATION:
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;  APPLICANT: Mintz, Liat
;  APPLICANT:  Xie, Hanqing
;  APPLICANT:  Dahari, Dvir
;  APPLICANT:  Levanon, Erez
;  APPLICANT:  Freilich, Shiri
;  APPLICANT:  Beck, Nili
;  APPLICANT:  Zhu, Wei-Yong
;  APPLICANT:  Wasserman, Alon
;  APPLICANT:  Hermesh, Chen
;  APPLICANT:  Azar, Idit
;  APPLICANT:  Bernstein, Jeanne
;  TITLE OF INVENTION: METHODS AND SYSTEMS USEFUL FOR ANNOTATING BIOMOLECULAR SEQUENCES
;  FILE REFERENCE: 02/23929
;  CURRENT APPLICATION NUMBER: US/11/443,428A
;  CURRENT FILING DATE:  2006-05-31
;  NUMBER OF SEQ ID NOS: 1034312
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 819823
;   LENGTH: 192
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-11-443-428A-819823

  Query Match             100.0%;  Score 882;  DB 6;  Length 192;
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Search completed: December 14, 2010, 11:32:16
Job time : 142.65 secs
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SCORE Search Results Details for Application 09556178 and Search Result 20101214_103255_us-09-556-178-5.rai.

Score Home Page Retrieve Application List SCORE System Overview SCORE FAQ Comments / Suggestions

This page gives you Search Results detail for the Application 09556178 and Search Result 20101214_103255_us-09-556-178-5.rai.

Go Back to previous page

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                        GenCore version 6.3
                  Copyright (c) 1993 - 2010  Biocceleration Ltd.


OM protein - protein search, using sw model

Run on:          December 14, 2010, 11:24:20 ; Search time 25 Seconds
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Title:           US-09-556-178-5
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Searched:        2170800 seqs, 396181022 residues

Total number of hits satisfying chosen parameters:      2170800

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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Database :        Issued_Patents_AA:*
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Result           Query
   No.    Score  Match Length DB  ID                          Description
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42	252	28.6	126	3	US-11-443-428A-819822	Sequence 819822,
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ALIGNMENTS

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US-08-967-364-5
; Sequence 5, Application US/08967364
; Patent No. 5989859
;  GENERAL INFORMATION:
;    APPLICANT:  Bandman, Olga
;    APPLICANT:  Lal, Preeti
;    APPLICANT:  Guegler, Karl J.
;    APPLICANT:  Shah, Purvi
;    APPLICANT:  Corley, Neil C.
;    TITLE OF INVENTION:  VESICLE TRAFFICKING PROTEINS
;    NUMBER OF SEQUENCES:  9
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Incyte Pharmaceuticals, Inc.
;      STREET:  3174 Porter Dr.
;      CITY:  Palo Alto
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  94304
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/967,364
;      FILING DATE:  No. 5989859ember 7, 1997
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;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Cerrone, Michael C.
;      REGISTRATION NUMBER:  39,132
;      REFERENCE/DOCKET NUMBER:  PF-0417 US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  650-855-0555
;      TELEFAX:  650-845-4166
;  INFORMATION FOR SEQ ID NO:  5:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  177 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    IMMEDIATE SOURCE:
;      LIBRARY:  HEAONOT03
;      CLONE:  3086794
US-08-967-364-5

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Qy        121 LFLAVDEIVDGGVILESDPQQVVHRVALRGEDVPLTEQTVSQVLQSAKEQIKWSLLR 177
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Db        121 LFLAVDEIVDGGVILESDPQQVVHRVALRGEDVPLTEQTVSQVLQSAKEQIKWSLLR 177


RESULT 2
US-09-368-408-5
; Sequence 5, Application US/09368408
; Patent No. 6071703
;  GENERAL INFORMATION:
;    APPLICANT:  Bandman, Olga
;    APPLICANT:  Lal, Preeti
;    APPLICANT:  Guegler, Karl J.
;    APPLICANT:  Shah, Purvi
;    APPLICANT:  Corley, Neil C.
;    TITLE OF INVENTION:  VESICLE TRAFFICKING PROTEINS
;    NUMBER OF SEQUENCES:  9
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Incyte Pharmaceuticals, Inc.
;      STREET:  3174 Porter Dr.
;      CITY:  Palo Alto
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  94304
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/368,408
;      FILING DATE:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/967,364
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;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Cerrone, Michael C.
;      REGISTRATION NUMBER:  39,132
;      REFERENCE/DOCKET NUMBER:  PF-0417 US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  650-855-0555
;      TELEFAX:  650-845-4166
;  INFORMATION FOR SEQ ID NO:  5:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  177 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    IMMEDIATE SOURCE:
;      LIBRARY:  HEAONOT03
;      CLONE:  3086794
US-09-368-408-5

  Query Match             100.0%;  Score 882;  DB 2;  Length 177;
  Best Local Similarity   100.0%;
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Qy         61 LLEGLTVVYKSSIDLYFYVIGSSYENELMLMAVLNCLFDSLSQMLRKNVEKRALLENMEG 120
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Db         61 LLEGLTVVYKSSIDLYFYVIGSSYENELMLMAVLNCLFDSLSQMLRKNVEKRALLENMEG 120

Qy        121 LFLAVDEIVDGGVILESDPQQVVHRVALRGEDVPLTEQTVSQVLQSAKEQIKWSLLR 177
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Db        121 LFLAVDEIVDGGVILESDPQQVVHRVALRGEDVPLTEQTVSQVLQSAKEQIKWSLLR 177


RESULT 3
US-11-443-428A-819809
; Sequence 819809, Application US/11443428A
; Patent No. 7745391
; GENERAL INFORMATION:
;  APPLICANT: Mintz, Liat
;  APPLICANT:  Xie, Hanqing
;  APPLICANT:  Dahari, Dvir
;  APPLICANT:  Levanon, Erez
;  APPLICANT:  Freilich, Shiri
;  APPLICANT:  Beck, Nili
;  APPLICANT:  Zhu, Wei-Yong
;  APPLICANT:  Wasserman, Alon
;  APPLICANT:  Hermesh, Chen
;  APPLICANT:  Azar, Idit
;  APPLICANT:  Bernstein, Jeanne
;  TITLE OF INVENTION: METHODS AND SYSTEMS USEFUL FOR ANNOTATING BIOMOLECULAR SEQUENCES
;  FILE REFERENCE: 02/23929
;  CURRENT APPLICATION NUMBER: US/11/443,428A
;  CURRENT FILING DATE:  2006-05-31
;  NUMBER OF SEQ ID NOS: 1034312
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 819809
;   LENGTH: 177
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-11-443-428A-819809

  Query Match             100.0%;  Score 882;  DB 3;  Length 177;
  Best Local Similarity   100.0%;
  Matches  177;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
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Qy          1 MEALILEPSLYTVKAILILDNDGDRLFAKYYDDTYPSVKEQKAFEKNIFNKTHRTDSEIA 60
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Qy         61 LLEGLTVVYKSSIDLYFYVIGSSYENELMLMAVLNCLFDSLSQMLRKNVEKRALLENMEG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LLEGLTVVYKSSIDLYFYVIGSSYENELMLMAVLNCLFDSLSQMLRKNVEKRALLENMEG 120

Qy        121 LFLAVDEIVDGGVILESDPQQVVHRVALRGEDVPLTEQTVSQVLQSAKEQIKWSLLR 177
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Db        121 LFLAVDEIVDGGVILESDPQQVVHRVALRGEDVPLTEQTVSQVLQSAKEQIKWSLLR 177


RESULT 4
US-11-443-428A-819804
; Sequence 819804, Application US/11443428A
; Patent No. 7745391
; GENERAL INFORMATION:
;  APPLICANT: Mintz, Liat
;  APPLICANT:  Xie, Hanqing
;  APPLICANT:  Dahari, Dvir
;  APPLICANT:  Levanon, Erez
;  APPLICANT:  Freilich, Shiri
;  APPLICANT:  Beck, Nili
;  APPLICANT:  Zhu, Wei-Yong
;  APPLICANT:  Wasserman, Alon
;  APPLICANT:  Hermesh, Chen
;  APPLICANT:  Azar, Idit
;  APPLICANT:  Bernstein, Jeanne
;  TITLE OF INVENTION: METHODS AND SYSTEMS USEFUL FOR ANNOTATING BIOMOLECULAR SEQUENCES
;  FILE REFERENCE: 02/23929
;  CURRENT APPLICATION NUMBER: US/11/443,428A
;  CURRENT FILING DATE:  2006-05-31
;  NUMBER OF SEQ ID NOS: 1034312
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 819804
;   LENGTH: 192
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-11-443-428A-819804

  Query Match             100.0%;  Score 882;  DB 3;  Length 192;
  Best Local Similarity   100.0%;
  Matches  177;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MEALILEPSLYTVKAILILDNDGDRLFAKYYDDTYPSVKEQKAFEKNIFNKTHRTDSEIA 60
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Qy         61 LLEGLTVVYKSSIDLYFYVIGSSYENELMLMAVLNCLFDSLSQMLRKNVEKRALLENMEG 120
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Db         76 LLEGLTVVYKSSIDLYFYVIGSSYENELMLMAVLNCLFDSLSQMLRKNVEKRALLENMEG 135

Qy        121 LFLAVDEIVDGGVILESDPQQVVHRVALRGEDVPLTEQTVSQVLQSAKEQIKWSLLR 177
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Db        136 LFLAVDEIVDGGVILESDPQQVVHRVALRGEDVPLTEQTVSQVLQSAKEQIKWSLLR 192


RESULT 5
US-11-443-428A-819805
; Sequence 819805, Application US/11443428A
; Patent No. 7745391
; GENERAL INFORMATION:
;  APPLICANT: Mintz, Liat
;  APPLICANT:  Xie, Hanqing
;  APPLICANT:  Dahari, Dvir
```

```
;  APPLICANT:  Levanon, Erez
;  APPLICANT:  Freilich, Shiri
;  APPLICANT:  Beck, Nili
;  APPLICANT:  Zhu, Wei-Yong
;  APPLICANT:  Wasserman, Alon
;  APPLICANT:  Hermesh, Chen
;  APPLICANT:  Azar, Idit
;  APPLICANT:  Bernstein, Jeanne
;  TITLE OF INVENTION: METHODS AND SYSTEMS USEFUL FOR ANNOTATING BIOMOLECULAR SEQUENCES
;  FILE REFERENCE: 02/23929
;  CURRENT APPLICATION NUMBER: US/11/443,428A
;  CURRENT FILING DATE:  2006-05-31
;  NUMBER OF SEQ ID NOS: 1034312
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 819805
;   LENGTH: 192
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-11-443-428A-819805

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Qy        121 LFLAVDEIVDGGVILESDPQQVVHRVALRGEDVPLTEQTVSQVLQSAKEQIKWSLLR 177
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Db        136 LFLAVDEIVDGGVILESDPQQVVHRVALRGEDVPLTEQTVSQVLQSAKEQIKWSLLR 192


RESULT 6
US-11-443-428A-819806
; Sequence 819806, Application US/11443428A
; Patent No. 7745391
; GENERAL INFORMATION:
;  APPLICANT: Mintz, Liat
;  APPLICANT:  Xie, Hanqing
;  APPLICANT:  Dahari, Dvir
;  APPLICANT:  Levanon, Erez
;  APPLICANT:  Freilich, Shiri
;  APPLICANT:  Beck, Nili
;  APPLICANT:  Zhu, Wei-Yong
;  APPLICANT:  Wasserman, Alon
;  APPLICANT:  Hermesh, Chen
;  APPLICANT:  Azar, Idit
;  APPLICANT:  Bernstein, Jeanne
;  TITLE OF INVENTION: METHODS AND SYSTEMS USEFUL FOR ANNOTATING BIOMOLECULAR SEQUENCES
;  FILE REFERENCE: 02/23929
;  CURRENT APPLICATION NUMBER: US/11/443,428A
;  CURRENT FILING DATE:  2006-05-31
;  NUMBER OF SEQ ID NOS: 1034312
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 819806
;   LENGTH: 192
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-11-443-428A-819806

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Db        136 LFLAVDEIVDGGVILESDPQQVVHRVALRGEDVPLTEQTVSQVLQSAKEQIKWSLLR 192


RESULT 7
US-11-443-428A-819808
; Sequence 819808, Application US/11443428A
; Patent No. 7745391
; GENERAL INFORMATION:
;  APPLICANT: Mintz, Liat
;  APPLICANT:  Xie, Hanqing
;  APPLICANT:  Dahari, Dvir
;  APPLICANT:  Levanon, Erez
;  APPLICANT:  Freilich, Shiri
;  APPLICANT:  Beck, Nili
;  APPLICANT:  Zhu, Wei-Yong
;  APPLICANT:  Wasserman, Alon
;  APPLICANT:  Hermesh, Chen
;  APPLICANT:  Azar, Idit
;  APPLICANT:  Bernstein, Jeanne
;  TITLE OF INVENTION: METHODS AND SYSTEMS USEFUL FOR ANNOTATING BIOMOLECULAR SEQUENCES
;  FILE REFERENCE: 02/23929
;  CURRENT APPLICATION NUMBER: US/11/443,428A
;  CURRENT FILING DATE:  2006-05-31
;  NUMBER OF SEQ ID NOS: 1034312
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 819808
;   LENGTH: 192
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-11-443-428A-819808

  Query Match             100.0%;  Score 882;  DB 3;  Length 192;
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RESULT 8
US-11-443-428A-819810
; Sequence 819810, Application US/11443428A
; Patent No. 7745391
; GENERAL INFORMATION:
;  APPLICANT: Mintz, Liat
;  APPLICANT:  Xie, Hanqing
```

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;  APPLICANT:  Dahari, Dvir
;  APPLICANT:  Levanon, Erez
;  APPLICANT:  Freilich, Shiri
;  APPLICANT:  Beck, Nili
;  APPLICANT:  Zhu, Wei-Yong
;  APPLICANT:  Wasserman, Alon
;  APPLICANT:  Hermesh, Chen
;  APPLICANT:  Azar, Idit
;  APPLICANT:  Bernstein, Jeanne
;  TITLE OF INVENTION: METHODS AND SYSTEMS USEFUL FOR ANNOTATING BIOMOLECULAR SEQUENCES
;  FILE REFERENCE: 02/23929
;  CURRENT APPLICATION NUMBER: US/11/443,428A
;  CURRENT FILING DATE:  2006-05-31
;  NUMBER OF SEQ ID NOS: 1034312
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 819810
;   LENGTH: 192
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-11-443-428A-819810

  Query Match             100.0%;  Score 882;  DB 3;  Length 192;
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Db        136 LFLAVDEIVDGGVILESDPQQVVHRVALRGEDVPLTEQTVSQVLQSAKEQIKWSLLR 192


RESULT 9
US-11-443-428A-819816
; Sequence 819816, Application US/11443428A
; Patent No. 7745391
; GENERAL INFORMATION:
;  APPLICANT: Mintz, Liat
;  APPLICANT:  Xie, Hanqing
;  APPLICANT:  Dahari, Dvir
;  APPLICANT:  Levanon, Erez
;  APPLICANT:  Freilich, Shiri
;  APPLICANT:  Beck, Nili
;  APPLICANT:  Zhu, Wei-Yong
;  APPLICANT:  Wasserman, Alon
;  APPLICANT:  Hermesh, Chen
;  APPLICANT:  Azar, Idit
;  APPLICANT:  Bernstein, Jeanne
;  TITLE OF INVENTION: METHODS AND SYSTEMS USEFUL FOR ANNOTATING BIOMOLECULAR SEQUENCES
;  FILE REFERENCE: 02/23929
;  CURRENT APPLICATION NUMBER: US/11/443,428A
;  CURRENT FILING DATE:  2006-05-31
;  NUMBER OF SEQ ID NOS: 1034312
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 819816
;   LENGTH: 192
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-11-443-428A-819816

  Query Match             100.0%;  Score 882;  DB 3;  Length 192;
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  Best Local Similarity   100.0%;
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Db         16 MEALILEPSLYTVKAILILDNDGDRLFAKYYDDTYPSVKEQKAFEKNIFNKTHRTDSEIA 75

Qy         61 LLEGLTVVYKSSIDLYFYVIGSSYENELMLMAVLNCLFDSLSQMLRKNVEKRALLENMEG 120
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Db         76 LLEGLTVVYKSSIDLYFYVIGSSYENELMLMAVLNCLFDSLSQMLRKNVEKRALLENMEG 135

Qy        121 LFLAVDEIVDGGVILESDPQQVVHRVALRGEDVPLTEQTVSQVLQSAKEQIKWSLLR 177
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Db        136 LFLAVDEIVDGGVILESDPQQVVHRVALRGEDVPLTEQTVSQVLQSAKEQIKWSLLR 192


RESULT 10
US-11-443-428A-819818
; Sequence 819818, Application US/11443428A
; Patent No. 7745391
; GENERAL INFORMATION:
;  APPLICANT: Mintz, Liat
;  APPLICANT:  Xie, Hanqing
;  APPLICANT:  Dahari, Dvir
;  APPLICANT:  Levanon, Erez
;  APPLICANT:  Freilich, Shiri
;  APPLICANT:  Beck, Nili
;  APPLICANT:  Zhu, Wei-Yong
;  APPLICANT:  Wasserman, Alon
;  APPLICANT:  Hermesh, Chen
;  APPLICANT:  Azar, Idit
;  APPLICANT:  Bernstein, Jeanne
;  TITLE OF INVENTION: METHODS AND SYSTEMS USEFUL FOR ANNOTATING BIOMOLECULAR SEQUENCES
;  FILE REFERENCE: 02/23929
;  CURRENT APPLICATION NUMBER: US/11/443,428A
;  CURRENT FILING DATE:  2006-05-31
;  NUMBER OF SEQ ID NOS: 1034312
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 819818
;   LENGTH: 192
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-11-443-428A-819818

  Query Match             100.0%;  Score 882;  DB 3;  Length 192;
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  Matches  177;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MEALILEPSLYTVKAILILDNDGDRLFAKYYDDTYPSVKEQKAFEKNIFNKTHRTDSEIA 60
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Qy         61 LLEGLTVVYKSSIDLYFYVIGSSYENELMLMAVLNCLFDSLSQMLRKNVEKRALLENMEG 120
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RESULT 11
US-11-443-428A-819819
; Sequence 819819, Application US/11443428A
; Patent No. 7745391
; GENERAL INFORMATION:
;  APPLICANT: Mintz, Liat
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;  APPLICANT:  Xie, Hanqing
;  APPLICANT:  Dahari, Dvir
;  APPLICANT:  Levanon, Erez
;  APPLICANT:  Freilich, Shiri
;  APPLICANT:  Beck, Nili
;  APPLICANT:  Zhu, Wei-Yong
;  APPLICANT:  Wasserman, Alon
;  APPLICANT:  Hermesh, Chen
;  APPLICANT:  Azar, Idit
;  APPLICANT:  Bernstein, Jeanne
;  TITLE OF INVENTION: METHODS AND SYSTEMS USEFUL FOR ANNOTATING BIOMOLECULAR SEQUENCES
;  FILE REFERENCE: 02/23929
;  CURRENT APPLICATION NUMBER: US/11/443,428A
;  CURRENT FILING DATE:  2006-05-31
;  NUMBER OF SEQ ID NOS: 1034312
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 819819
;   LENGTH: 192
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-11-443-428A-819819

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RESULT 12
US-11-443-428A-819821
; Sequence 819821, Application US/11443428A
; Patent No. 7745391
; GENERAL INFORMATION:
;  APPLICANT: Mintz, Liat
;  APPLICANT:  Xie, Hanqing
;  APPLICANT:  Dahari, Dvir
;  APPLICANT:  Levanon, Erez
;  APPLICANT:  Freilich, Shiri
;  APPLICANT:  Beck, Nili
;  APPLICANT:  Zhu, Wei-Yong
;  APPLICANT:  Wasserman, Alon
;  APPLICANT:  Hermesh, Chen
;  APPLICANT:  Azar, Idit
;  APPLICANT:  Bernstein, Jeanne
;  TITLE OF INVENTION: METHODS AND SYSTEMS USEFUL FOR ANNOTATING BIOMOLECULAR SEQUENCES
;  FILE REFERENCE: 02/23929
;  CURRENT APPLICATION NUMBER: US/11/443,428A
;  CURRENT FILING DATE:  2006-05-31
;  NUMBER OF SEQ ID NOS: 1034312
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 819821
;   LENGTH: 192
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-11-443-428A-819821
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Db        136 LFLAVDEIVDGGVILESDPQQVVHRVALRGEDVPLTEQTVSQVLQSAKEQIKWSLLR 192


RESULT 13
US-11-443-428A-819823
; Sequence 819823, Application US/11443428A
; Patent No. 7745391
; GENERAL INFORMATION:
;  APPLICANT: Mintz, Liat
;  APPLICANT:  Xie, Hanqing
;  APPLICANT:  Dahari, Dvir
;  APPLICANT:  Levanon, Erez
;  APPLICANT:  Freilich, Shiri
;  APPLICANT:  Beck, Nili
;  APPLICANT:  Zhu, Wei-Yong
;  APPLICANT:  Wasserman, Alon
;  APPLICANT:  Hermesh, Chen
;  APPLICANT:  Azar, Idit
;  APPLICANT:  Bernstein, Jeanne
;  TITLE OF INVENTION: METHODS AND SYSTEMS USEFUL FOR ANNOTATING BIOMOLECULAR SEQUENCES
;  FILE REFERENCE: 02/23929
;  CURRENT APPLICATION NUMBER: US/11/443,428A
;  CURRENT FILING DATE:  2006-05-31
;  NUMBER OF SEQ ID NOS: 1034312
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 819823
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;   ORGANISM: Homo sapiens
US-11-443-428A-819823

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RESULT 14
US-11-443-428A-819825
; Sequence 819825, Application US/11443428A
; Patent No. 7745391
; GENERAL INFORMATION:
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;  APPLICANT: Mintz, Liat
;  APPLICANT:  Xie, Hanqing
;  APPLICANT:  Dahari, Dvir
;  APPLICANT:  Levanon, Erez
;  APPLICANT:  Freilich, Shiri
;  APPLICANT:  Beck, Nili
;  APPLICANT:  Zhu, Wei-Yong
;  APPLICANT:  Wasserman, Alon
;  APPLICANT:  Hermesh, Chen
;  APPLICANT:  Azar, Idit
;  APPLICANT:  Bernstein, Jeanne
;  TITLE OF INVENTION: METHODS AND SYSTEMS USEFUL FOR ANNOTATING BIOMOLECULAR SEQUENCES
;  FILE REFERENCE: 02/23929
;  CURRENT APPLICATION NUMBER: US/11/443,428A
;  CURRENT FILING DATE:  2006-05-31
;  NUMBER OF SEQ ID NOS: 1034312
;  SOFTWARE: PatentIn version 3.1
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;   ORGANISM: Homo sapiens
US-11-443-428A-819825

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RESULT 15
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; Sequence 819807, Application US/11443428A
; Patent No. 7745391
; GENERAL INFORMATION:
;  APPLICANT: Mintz, Liat
;  APPLICANT:  Xie, Hanqing
;  APPLICANT:  Dahari, Dvir
;  APPLICANT:  Levanon, Erez
;  APPLICANT:  Freilich, Shiri
;  APPLICANT:  Beck, Nili
;  APPLICANT:  Zhu, Wei-Yong
;  APPLICANT:  Wasserman, Alon
;  APPLICANT:  Hermesh, Chen
;  APPLICANT:  Azar, Idit
;  APPLICANT:  Bernstein, Jeanne
;  TITLE OF INVENTION: METHODS AND SYSTEMS USEFUL FOR ANNOTATING BIOMOLECULAR SEQUENCES
;  FILE REFERENCE: 02/23929
;  CURRENT APPLICATION NUMBER: US/11/443,428A
;  CURRENT FILING DATE:  2006-05-31
;  NUMBER OF SEQ ID NOS: 1034312
;  SOFTWARE: PatentIn version 3.1
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;   ORGANISM: Homo sapiens
US-11-443-428A-819807
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SCORE Search Results Details for Application 09556178 and Search Result 20101214_103257_us-09-556-178-5.rapbn.

Score Home Page Retrieve Application List SCORE System Overview SCORE FAQ Comments / Suggestions

This page gives you Search Results detail for the Application 09556178 and Search Result 20101214_103257_us-09-556-178-5.rapbn.

Go Back to previous page

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                        GenCore version 6.3
                  Copyright (c) 1993 - 2010  Biocceleration Ltd.


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; Sequence 1740, Application US/12800898
; Publication No. US20100303822A1
; GENERAL INFORMATION:
;  APPLICANT: MASIGNANI, Vega
;  APPLICANT:  ARICO, Maria
;  TITLE OF INVENTION: POLYPEPTIDES FROM NON-TYPEABLE HAEMOPHILUS INFLUENZAE
;  FILE REFERENCE: PP022930.0003
;  CURRENT APPLICATION NUMBER: US/12/800,898
;  CURRENT FILING DATE:  2010-05-25
;  PRIOR APPLICATION NUMBER: US/11/596,557
;  PRIOR FILING DATE: 2006-11-14
;  PRIOR APPLICATION NUMBER: GB-0410866.8
;  PRIOR FILING DATE: 2004-05-14
;  NUMBER OF SEQ ID NOS: 5095
;  SOFTWARE: SeqWin99, version 1.0.4
; SEQ ID NO 1740
;   LENGTH: 379
;   TYPE: PRT
;   ORGANISM: Haemophilus influenzae
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;   OTHER INFORMATION: Name: NTH0958
US-12-800-898-1740

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